



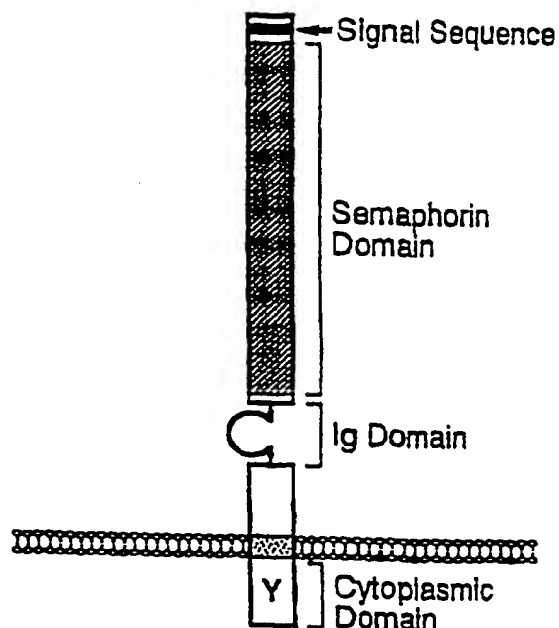
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(54) Title: CD100 ANTIGEN AND USES THEREFOR

(57) Abstract

Isolated nucleic acid molecules encoding novel CD100 molecules which stimulate a leukocyte response, such as a B cell response, including B cell aggregation, B cell differentiation, B cell survival, and/or T cell proliferation are disclosed. These novel molecules have a certain homology to semaphorins, proteins which are growth cone guidance molecules that are critical for guiding growing axons of neurons to their targets. In addition to isolated nucleic acid molecules, antisense nucleic acid molecules, recombinant expression vectors containing a nucleic acid molecule of the invention, host cells into which the expression vectors have been introduced are also described. The invention further provides isolated CD100 proteins, fusion proteins and active fragments thereof. Diagnostic and therapeutic methods utilizing compositions of the invention are also provided.

Human CD100

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- 1 -

CD100 ANTIGEN AND USES THEREFOR

Background of the Invention

Induction of a humoral response is important in host defense, for example, in fighting infections by pathogens. A humoral response is mediated by B cells, but requires the help of other cells, such as T cells. Development of a humoral response is a multistage process which occurs primarily in secondary lymphoid tissues.

Resting B cells circulate in the blood, pass through secondary lymphoid tissues, such as lymph nodes, Peyer's patches, spleen and tonsils, where they come into contact with trapped antigens. B cells recognizing a specific antigen through their surface immunoglobulins process the antigen and enter the T cell rich paracortical regions below the outer layer, or cortex, of lymphoid tissues. Some of the T cells in this region have been activated through contact with antigen presenting cells. These T cells in turn promote B cell activation by direct contact with the B cells via interaction of cell surface molecules and by the secretion of T cell-specific cytokines, such as IL-2, IL-4, and IL-5. This cell-cell interaction between T and B cells or production of T cell specific cytokines induces B cells to migrate into B cell follicles. In these follicles, the B cells interact with follicular dendritic cells having antigen-antibody complexes on their surface resulting in the formation of a germinal center. B cells in germinal centers undergo active proliferation, affinity maturation, and differentiation into memory B cells or antibody secreting plasma cells. Thus, whereas antibody-secreting plasma cells produce antibodies to fight infections, memory B cells assure a more rapid response to subsequent exposure to the same antigen.

Some molecules involved in the induction of B-cell proliferation and differentiation have been identified. In addition to cytokines produced in large part by activated T cells, crosslinking of specific B cell surface molecules also provide such signals (Clark E. A. et al, (1994), *Nature* 367, 425). One such B cell surface molecule is CD40. CD40 is a 45-50 kD protein expressed on activated B cells. Valle et al., (1989), *Eur. J. Immunol.*, 19:1463-1467; Gordon et al., (1988), *J. Immunol.*, 140:1425-1430; Gruber et al., (1989), *J. Immunol.*, 142: 4144-4152. Crosslinking of CD40 with antibodies or with its natural ligand, CD40L, also termed gp39, together with other stimulatory signals induces B cell proliferation and antibody production. Armitage et al., (1992), *Nature*, 357:80-82 ; Hollenbaugh et al., (1992), *EMBO J.*, 11:4313-4319.

T cells are not only required for providing help to B cells, but also play a major role in cellular immune responses, such as in delayed type hypersensitivity reactions and in cytotoxicity. To exert their activity, T cells must be activated. To induce antigen-specific T cell activation and clonal expansion, two signals provided by antigen-presenting cells (APCs) must be delivered to the surface of resting T lymphocytes (Jenkins, M. and Schwartz, R. (1987) *J. Exp. Med.* 165, 302-319; Mueller, D.L., et al. (1990) *J. Immunol.* 144, 3701-3709; Williams, I.R. and Unanue, E.R. (1990) *J. Immunol.* 145, 85-93). The

- 2 -

first signal, which confers specificity to the immune response, is mediated via the T cell receptor (TCR) following recognition of foreign antigenic peptide presented in the context of the major histocompatibility complex (MHC). The second signal, termed costimulation, induces T cells to proliferate and become functional (Schwartz, R.H. (1990) *Science* 248, 1349-1356). Costimulation is neither antigen-specific, nor MHC restricted and is thought to be provided by one or more distinct cell surface molecules expressed by APCs (Jenkins, M.K., et al. (1988) *J. Immunol.* 140, 3324-3330; Linsley, P.S., et al. (1991) *J. Exp. Med.* 173, 721-730; Gimmi, C.D., et al., (1991) *Proc. Natl. Acad. Sci. USA.* 88, 6575-6579; Young, J.W., et al. (1992) *J. Clin. Invest.* 90, 229-237; Koulova, L., et al. (1991) *J. Exp. Med.* 173, 759-762; Reiser, H., et al. (1992) *Proc. Natl. Acad. Sci. USA.* 89, 271-275; van-Seventer, G.A., et al. (1990) *J. Immunol.* 144, 4579-4586; LaSalle, J.M., et al., (1991) *J. Immunol.* 147, 774-80; Dustin, M.I., et al., (1989) *J. Exp. Med.* 169, 503; Armitage, R.J., et al. (1992) *Nature* 357, 80-82; Liu, Y., et al. (1992) *J. Exp. Med.* 175, 437-445). B7-1 and B7-2 are two such costimulatory molecules which interact with CD28 and CTLA4 on T cells (Linsley, P.S., et al., (1991) *J. Exp. Med.* 173, 721-730; Gimmi, C.D., et al., (1991) *Proc. Natl. Acad. Sci. USA.* 88, 6575-6579; Koulova, L., et al., (1991) *J. Exp. Med.* 173, 759-762; Reiser, H., et al. (1992) *Proc. Natl. Acad. Sci. USA.* 89, 271-275; Linsley, P.S. et al. (1990) *Proc. Natl. Acad. Sci. USA.* 87, 5031-5035; Freeman, G.J. et al. (1991) *J. Exp. Med.* 174, 625-631; Freeman, G.J. et al. (1993) *Science* 262:909-911; Azuma, M. et al. (1993) *Nature* 366:76-79; and Freeman, G.J. et al. (1993) *J. Exp. Med.* 178:2185-2192). Though the molecules B7-1 and B7-2 play a critical role in costimulation of T cell, there is some evidence that additional molecules can provide a costimulatory signal to T cells.

Previous studies demonstrated that several antibodies recognized a 150kD cell-surface homodimer, termed CD100, that is expressed on a number of hematopoietic cells including B and T lymphocytes, granulocytes, monocytes and natural killer cells, but not on eosinophils, platelets, erythrocytes or hematopoietic progenitor cells (Bougeret, C. et al., (1992), *J. Immunol.* 148, 318; Herold, C., et al., Eds., (Oxford University Press, Oxford, 1995), *Leucocyte Typing V*, S. F. Schlossman, et al., Eds. vol. 1, pp. 52). These studies indicated that CD100 expression on resting T cells increases on T cells after phytohemagglutinin activation (Bougeret, C. et al., (1992), *J. Immunol.* 148, 318). In addition, it has been reported that crosslinking of CD100 provides a costimulatory signal to T cells, indicating that this molecule may be involved in T cell activation and clonal expansion (Herold C. et al., (1994), *Int. Immunol.* 7, 1). However, the role of CD100, in particular its role on B lymphocytes is unknown.

Summary of the Invention

This invention provides isolated nucleic acid molecules encoding a CD100 antigen. Such nucleic acid molecules (e.g., cDNAs) have a nucleotide sequence encoding a CD100 antigen or biologically active portions thereof, such as a peptide having a CD100 activity. In

- 3 -

a preferred embodiment, the isolated nucleic acid molecule has a nucleotide sequence shown in Figure 1, SEQ ID NO: 1, or a portion thereof such as the coding region of the nucleotide sequence of Figure 1, SEQ ID NO: 1. Other preferred nucleic acid molecules encode a protein having the amino acid sequence of Figure 2, SEQ ID NO: 2. In another preferred embodiment, the isolated nucleic acid molecule has a nucleotide sequence shown in Figure 12, SEQ ID NO: 8 and/or encodes a protein having an amino acid sequence shown in Figure 14, SEQ ID NO: 9. Nucleic acid molecules derived from hematopoietic cells (e.g., a naturally-occurring nucleic acid molecule found in an activated lymphocyte) which hybridize under stringent conditions to the nucleotide sequence shown in Figure 1, SEQ ID NO: 1 or Figure 12, SEQ ID NO: 8 are also within the scope of the invention.

In another embodiment, the isolated nucleic acid molecule is a nucleotide sequence encoding a protein having an amino acid sequence which is at least about 80%, preferably at least about 85%, more preferably at least about 90% and most preferably at least about 95-99% overall amino acid sequence identity with an amino acid sequence shown in Figure 2, SEQ ID NO: 2. This invention further pertains to nucleic acid molecules which encode a protein which includes a semaphorin domain having an amino acid sequence at least about 80%, preferably at least about 90%, more preferably at least about 95-99% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2. Also within the scope of this invention are nucleic acid molecules which encode a protein which includes an extracellular domain having an amino acid sequence at least 80%, preferably at least 90%, more preferably at least 95-99% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2.

Nucleic acid molecules encoding proteins which include a semaphorin domain having an amino acid sequence at least about 60% (preferably at least about 70%, 80%, 90%, or 95-99%) identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2 and an immunoglobulin-like domain having an amino acid sequence at least about 50% (preferably at least about 60%, 70%, 80%, 90%, or 95-99%) identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2 are also within the scope of this invention. These nucleic acid molecules can encode proteins which optionally include a cytoplasmic domain having an amino acid sequence at least about 50% (preferably at least about 60%, 70%, 80%, 90%, or 95-99%) identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2.

Another aspect of this invention pertains to nucleic acid molecules encoding a CD100 fusion protein which includes a nucleotide sequence encoding a first peptide having an amino acid sequence at least about 80% (preferably at least about 90%, or 95-99%) identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2 and a nucleic acid sequence encoding a second peptide corresponding to a moiety that facilitates detection or purification of the molecules or that alter the solubility, binding affinity or valency of the first peptide, such as an immunoglobulin constant region.

- 4 -

In another embodiment, the isolated nucleic acid molecule has a nucleotide sequence encoding a peptide fragment of at least about 30 amino acid residues in length, preferably at least about 40 amino acid residues in length, and more preferably at least about 50 amino acid residues in length corresponding to an amino acid sequence shown in Figure 2, SEQ ID NO: 2. In a preferred embodiment, the peptide fragment has a CD100 activity.

Moreover, given the disclosure herein of a CD100-encoding cDNA sequence (e.g., SEQ ID NO: 1), antisense nucleic acid molecules (i.e., molecules which are complimentary to the coding strand of the CD100 cDNA sequence) are also provided by the invention.

Another aspect of the invention pertains to recombinant expression vectors containing the nucleic acid molecules of the invention and host cells into which such recombinant expression vectors have been introduced. In one embodiment, such a host cell is used to produce CD100 protein by culturing the host cell in a suitable medium. If desired, CD100 protein can then be isolated from the medium or the host cell.

Still another aspect of the invention pertains to isolated CD100 proteins and active fragments thereof, such as peptides having an activity of a CD100 antigen (e.g., at least one biological activity of CD100, such as the ability to stimulate a B cell response, for example, B cell aggregation or the ability to stimulate a T cell response, for example, T cell proliferation). The invention also provides an isolated preparation of a CD100 protein. In preferred embodiments, the CD100 protein comprises an amino acid sequence of Figure 2, SEQ ID NO: 2, or a mature CD100 protein lacking an amino-terminal signal sequence (e.g., a CD100 molecule having amino acid residues 22-862 or 24-862 of Figure 2, SEQ ID NO: 2 or having amino acid residues 22-861 or 24-861 of Figure 14, SEQ ID NO: 9). In other embodiments, the isolated CD100 protein comprises an amino acid sequence at least 80 % identical to an amino acid sequence of Figure 2, SEQ ID NO: 2 and, preferably has an activity of CD100 (e.g., at least one biological activity of CD100). Preferably, the protein is at least about 90 %, more preferably at least about 95 %, even more preferably at least about 98 % and most preferably at least about 99 % identical to the amino acid sequence of Figure 2, SEQ ID NO: 2.

This invention also pertains to isolated peptides which include a semaphorin domain having an amino acid sequence that is at least about 60% (preferably at least about 70%, 80%, 90%, or 95-99%) identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2) and an immunoglobulin-like domain having an amino acid sequence that is at least 50% (preferably at least about 60%, 70%, 80%, 90%, or 95-99%) identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2). These peptides can optionally include a cytoplasmic domain having an amino acid sequence that is at least about 50% identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).

- 5 -

The invention also provides for a CD100 fusion protein comprising a first peptide having an amino acid sequence at least about 80% identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2) and a second peptide corresponding to a moiety that alters the solubility, binding affinity or valency of the first peptide. In preferred
5 embodiments, the fusion protein comprises an extracellular domain of a CD100 antigen. In yet another embodiment, the fusion protein comprises a semaphorin domain of a CD100 antigen.

Peptides comprising a fragment of at least about 30 amino acids, a fragment of at least about 40 amino acids, a fragment of at least about 50 amino acids, or longer fragments
10 of the sequence shown in Figure 2 (SEQ ID NO: 2) are also within the scope of the invention. The peptide fragments preferably have a CD100 activity.

A CD100 protein of the invention can be incorporated into a pharmaceutical composition which includes the protein (or active portion thereof) and a pharmaceutically acceptable carrier. In addition, vaccine compositions which include at least one antigen and
15 a first agent which stimulates a CD100 ligand-associated signal in a cell, such as a leukocyte, e.g., a B cell or a T cell, are also within the scope of this invention. Such vaccine compositions can further include a second agent which stimulates a CD40-associated signal in a cell (e.g., a B cell).

The CD100 protein of the invention and agents which modulate a CD100 ligand-associated signal in a cell, such as a leukocyte can be used to modulate leukocyte responses
20 *in vitro* or *in vivo*. In one embodiment, the invention provides a method for stimulating a CD100 ligand-associated signal in a B cell by contacting the cell with an agent that stimulates a CD100 ligand-associated signal. Such an agent can be, for example, a stimulatory form of a CD100 antigen (e.g., a soluble CD100 protein). Additional agents,
25 such as an agent which provides a CD40 associated signal in the B cell can be used to stimulate a B cell response.

In another embodiment, a CD100 ligand-associated signal is inhibited to thereby inhibit a response by a B cell. In this embodiment, an agent which interacts with CD100, such as an anti-CD100 antibody can be used to inhibit a response by a B cell such as aggregation or
30 differentiation. The methods of the invention for modulating B cell responses by manipulating the interaction of CD100 with its ligand can be applied *in vitro* (e.g., with cells in culture) or *in vivo*, wherein an agent that modulates CD100 and/or CD100 ligand is administered to the subject.

The invention further provides methods for modulating a T cell response
35 comprising contacting a T cell with an agent which modulates a CD100 ligand-associated signal in the T cell. A T cell response is preferably T cell proliferation. The method also preferably includes contacting the T cell with a primary activation agent, such as an antibody to CD3 or at least one antigen.

- 6 -

Additional methods for modulating an interaction between immune cells and nerve cells in a subject by administering an amount of an agent which modulates a CD100 signal in the subject as well as methods for modulating and/or guiding axonal growth by contacting neurons with a modulating form of CD100, such that such that axonal growth is modulated and/or guided are also within the scope of the invention.

Brief Description of the Drawings

Figure 1 is the nucleotide sequence of a 4.2 kb cDNA encoding full length human CD100 (SEQ ID NO: 1) and the predicted amino acid sequence encoded by the cDNA (SEQ ID NO: 2).

Figure 2 is the predicted full length amino acid sequence of human CD100 (SEQ ID NO: 2) aligned for comparison to the semaphorin and Ig domains of Human semaphorin III (H-sema III) (SEQ ID NO: 3) and Mouse semaphorin C (M-Sema C) (SEQ ID NO: 4). The regions of identity are boxed. The putative hydrophobic region of the signal sequence is underlined; the sema domain is delimited by *; the gray box indicates an Ig-like domain; the transmembrane region is double-underlined; and the putative tyrosine phosphorylation site KPALTGY (SEQ ID NO: 5) (MAC Pattern: GenBank accession number PS00007) in the cytoplasmic tail is boxed.

Figure 3 is a schematic representation of the structure of human CD100 indicating the different domains and the tyrosine phosphorylation site (Y).

Figure 4 represents a sequence comparison between the amino acid sequence of collapsin 4 (top sequence) and the amino acid sequence of a fragment of human CD100 (bottom sequence).

Figure 5 is a graphic representation of the result of flow cytometry analyses of COS cells transiently transfected with a CD100 cDNA (CD100), pCDM8 vector alone (Vector), and B7-1 cDNA (B7-1) and stained with the anti-CD100 antibodies BD16, F93G2, and BB18; and with the isotype matched B7-1 antibody B1.1.

Figure 6 are photographs depicting human splenic B cells cultured with mock transfected NIH-3T3 cells (t-mock) (Figure 6a); CD40L transfected NIH-3T3 cells (t-CD40L; Figures 6b and e); 50% mock transfected and 50% CD40L transfected NIH-3T3 cells (t-mock/t-CD40L) (Figure 6c), CD100 transfected NIH-3T3 cells (t-CD100) (Figure 6d); and 50% CD100 transfected and 50% CD40L transfected NIH-3T3 cells (t-CD100/t-CD40L) (Figure 6f), showing that CD100 stimulates B cell homotypic aggregation and that this effect synergizes with CD40 stimulation.

Figure 7 depicts a histogram showing the number of viable human B cells ($\times 10^6$) after incubation of 10^6 B cells for 72 hours with mock transfected NIH-3T3 cells (t-mock); CD100 transfected NIH-3T3 cells (t-CD100); CD40 transfected NIH-3T3 cells (t-CD40); 50% mock transfected and 50% CD40L transfected NIH-3T3 cells (t-mock/t-CD40L); and 50% CD100 transfected and 50% CD40L transfected NIH-3T3 cells indicating that CD100

- 7 -

and CD40L stimulation prolong B cell survival and that CD100 and CD40L synergistically stimulate B cell survival.

Figure 8 is a graphic representation of a two color FACS analysis performed with anti-CD19 and anti-CD23 antibodies of human splenic B cells performed after 72 hours of co-culture with t-mock/t-CD40L cells or t-CD100/t-CD40L showing that CD100 reduces expression of CD40L-induced CD23 expression.

Figure 9 depicts the results of proliferation assays of CD4+ T cells incubated in media alone, with an anti-CD3 antibody, with an anti-CD3 antibody and NIH-3T3 cells transfected with a B7-1 cDNA (t-B7-1), with an anti-CD3 antibody and NIH-3T3 cells transfected with a B7-2 cDNA (t-B7-2), and with an anti-CD3 antibody and NIH-3T3 cells transfected with a CD100 cDNA (t-CD100) showing that CD100 is a T cell costimulatory molecule.

Figure 10 depicts the results of proliferation assays of CD4+ T cells incubated with an anti-CD3 antibody and 2×10^4 t-B7-1 cells and 0, 1×10^4 , 2×10^4 , or 3×10^4 t-B7-1 or t-CD100 cells.

Figure 11 depicts the results of proliferation assays of CD4+ T cells incubated with an anti-CD3 antibody and 2×10^4 t-B7-2 cells and 0, 1×10^4 , 2×10^4 , or 3×10^4 t-B7-2 or t-CD100 cells.

Figure 12 is the nucleotide sequence of a cDNA encoding murine CD100 (SEQ ID NO: 8).

Figure 13 shows a sequence comparison between the nucleic acid sequence of the open reading frame of human CD100 (bottom sequence, termed cd100, SEQ ID NO: 22 and nucleotides 88-2673 of SEQ ID NO: 1) and mouse CD100 (top sequence, termed mod2c-106, nucleotides 434-3016 of SEQ ID NO: 8). Hyphens indicate identical nucleotides and dots indicate gaps, i.e., nucleotides absent from one of the two sequences.

Figure 14 is the amino acid sequence of mouse CD100 (SEQ ID NO: 9).

Figure 15 shows an alignment of the amino acid sequences of portions of mouse and human CD100 proteins: a portion comprising the signal peptide domain (SEQ ID NO: 10 and SEQ ID NO: 11, respectively); a portion comprising the sema domain (SEQ ID NO: 12 and SEQ ID NO: 13, respectively); a portion comprising the Ig-like domain (SEQ ID NO: 14 and SEQ ID NO: 15, respectively); a portion comprising the stalk domain (SEQ ID NO: 16 and SEQ ID NO: 17, respectively); a portion comprising the transmembrane domain (SEQ ID NO: 18 and SEQ ID NO: 19, respectively); and a portion comprising the cytoplasmic domain (SEQ ID NO: 20 and SEQ ID NO: 21, respectively). Bars indicate identical amino acids and stars indicate conservative amino acid substitutions.

- 8 -

Detailed Description of the Invention

The invention pertains to novel CD100 antigens, or active portion thereof which are capable of stimulating a leukocyte response, such as a B cell response. The B cell response can be B cell aggregation. These CD100 antigens are preferably capable of inducing differentiation of B cells and/or are capable of increasing the viability of B cells and, thus, are involved in germinal center development (e.g., affinity maturation of antibodies). Even more preferred CD100 antigens are capable of stimulating a T cell response, such as T cell proliferation. A particularly preferred CD100 antigen is a human CD100 antigen which is expressed on various hematopoietic cells including activated T and B cells. The CD100 antigens of the invention are capable of synergizing with a CD40 ligand (e.g., gp39) to enhance stimulation of homotypic B cell aggregation and cell viability. Thus, the CD100 antigen amplifies a response of B cells to CD40. CD100 also modifies the response of B cells to CD40 by reducing the level of expression of CD23, a cell surface protein which is upregulated in response to stimulation with a CD40 ligand.

CD100 protein is a homodimeric transmembrane protein consisting of two polypeptide chains of about 150 kDa. The amino acid sequence of a polypeptide chain of human CD100 is shown in Figure 2 (SEQ ID NO: 2). The amino acid sequence of a polypeptide chain of mouse CD100 is shown in Figure 14 (SEQ ID NO: 9). As used herein, the term "CD100" is intended to include the homodimeric protein as well as a single CD100 polypeptide chain.

Each polypeptide chain of CD100 consists of several domains, shown schematically in Figure 3, which consist essentially of a signal peptide domain, a semaphorin domain, an immunoglobulin-like (Ig-like) domain, a stalk domain, a transmembrane domain, and a cytoplasmic domain. These domains are further described below.

(a) **Signal peptide domain**

As defined in the art, a signal peptide domain typically comprises of a hydrophobic domain and has small amino acids (e.g., glycine and alanine) located at amino acid positions -1 and -3 (amino acid position 1 being defined as the first amino acid of the mature form of the protein). A hydrophobic domain of human CD100 is located at about amino acids 9 to about amino acid 20. Small amino acids can be found at positions 19 (Glycine), 21 (Alanine), and 23 (Alanine) of human CD100 (Figures 1 and 2). Accordingly, a putative signal peptide cleavage site is located between amino acids 21 (Alanine) and 22 (Methionine) of human CD100. A preferred putative signal peptide cleavage site is located between amino acids 23 (Alanine) and 24 (Phenylalanine) of human CD100. Thus, cleavage at the first putative signal peptide cleavage site would result in a mature human CD100 protein having amino acids 22 to 262 of SEQ ID NO: 2. Cleavage at the second putative signal peptide cleavage site would result in a mature human CD100 protein having amino acids 24 to 262 of SEQ ID NO: 2. Similarly, in mouse CD100, a first putative signal peptide cleavage site is located between amino acids 21 (Alanine) and 22

- 9 -

(Valine). Cleavage at this first putative signal peptide cleavage site would result in a mature murine CD100 protein having amino acids 22 to 261 of SEQ ID NO: 9. A second putative signal peptide cleavage site in mouse CD100 is located between amino acids 23 (Alanine) and 24 (Phenylalanine). Cleavage at this second putative signal peptide cleavage site would result in a mature murine CD100 protein having amino acids 24 to 261 of SEQ ID NO: 9.

Various techniques can be used to identify which of the putative signal peptide cleavage sites (among those identified above and others) is in fact the site of cleavage of the mature CD100 protein in vivo. For, example, a CD100 protein on a cell surface can be isolated and the amino acid sequence of the N-terminus can be determined. Isolation of the CD100 protein must be done in conditions minimizing protein degradation by proteolytic enzymes.

(b) Semaphorin domain

As defined in the art, a semaphorin (sema) domain is an extracellular domain of approximately 500 amino acid containing 14-16 cysteines found specifically in proteins belonging to the semaphorin protein family. Accordingly, the sema domain of human and mouse CD100 can be defined as including about amino acid 42 to about amino acid 553 of SEQ ID NO: 2 and SEQ ID NO: 9, respectively. However, additional amino acids flanking amino acids 42 to 553 and which have significant homology to the sema domain of semaphorin family members can also be part of the semaphorin domain. Similarly, the sema domain can also be defined as consisting of less than amino acids 42 to 553. All these fragments of CD100 are within the scope of the invention and intended to be included in the term "CD100 sema domain". A "CD100 sema domain includes about amino acids 42 to 553 of SEQ ID NO: 2 or SEQ ID NO: 9" is also intended to include portions of CD100 which can be defined as sema domains.

The phylogenetically conserved semaphorins have been characterized in insect, chicken, mouse and human nervous systems (Kolodkin A.L., et al., (1992), *Neuron* 9, 831; Luo Y. et al, (1993), *Cell* 75, 217; Kolodkin A. et al, (1993), *Cell* 75, 1389; Puschel, A. W., et al. (1995) *Neuron* 14:941; Messersmith, E.K et al. (1995) *Neuron* 14:949; published PCT patent application number PCT/US94/10151). Proteins having a semaphorin domain have also been found in vaccinia virus, variola virus (Kolodkin A. et al, (1993), *Cell* 75, 1389), and herpes virus (Ensser, A. and Fleckenstein, B.(1995) *J. Gen. Virol.* 76: 1063). However the viral semaphorins are only distantly related to the previously identified mammalian and insect semaphorins.

As shown in Figure 2, human CD100 shares certain structural features with H-Sema III and mouse Sema C (M-Sema C). H-Sema III and M-Sema C molecules contain the highly conserved 500 amino acid (aa) semaphorin (sema) domain followed by a C-2 type immunoglobulin-like (Ig) domain. Human CD100 shares 39% identity with H-sema III in

- 10 -

the sema domain and 33% identity in the Ig-like domain, whereas the rest of the protein is strikingly divergent. Human CD100 contains 15 of the 16 conserved sema domain cysteines and 9 putative N-linked glycosylation sites. However, CD100 differs from H-Sema III and M-Sema C in that CD100 is a membrane bound protein, whereas H-Sema III and M-Sema C are secreted proteins. Other semaphorins related to collapsin have been isolated from chicken brains (Luo et al. (1995) *Neuron* 14:1131) and partially characterized. The partial amino acid sequence of one of these proteins, collapsin 4 (SEQ ID NO: 6), shares about 78% amino acid identity with a 295 amino acid long C-terminal portion of the human CD100 sema domain (amino acid residues 228-522 of the sequence shown in Figure 2 (SEQ ID NO: 2). The sequence comparison is shown in Figure 4. It is unknown whether collapsin 4 is a secreted protein or a membrane bound protein and whether it contains an Ig-like domain.

The human CD100 antigen is the first membrane bound protein shown to have a semaphorin domain and an Ig-like domain. Furthermore, human CD100 is the only membrane bound semaphorin having a tyrosine phosphorylation site in the cytoplasmic domain (see below). Based on its structure, CD100 can be defined as being a class IV semaphorin.

Accordingly, preferred CD100 antigens within the scope of the invention include a semaphorin domain or active portion thereof. Some members of the Semaphorin family have been shown to function as secreted or transmembrane proteins growth cone guidance molecules which are critical for guiding axonal growth of neurons. Membrane bound semaphorins include the grasshopper G-Sema I (also termed G-Fas IV), the Tribolium T-Sema I and the Drosophila D-Sema I. These proteins have an additional stretch of about 80 amino acids in the extracellular domain, a transmembrane domain, and an 80 to 110 amino acid cytoplasmic domain. Secreted semaphorins include the Drosophila D-Sema II, the chicken Collapsin, the human H-Sema III, and the mouse Sema C proteins. Secreted semaphorins have an additional stretch of about 20 amino acids in the extracellular domain, a single immunoglobulin domain and a 70-120 amino acid C-terminal region.

At least some semaphorins are involved in the nervous system development. Neurons secreting semaphorins such as chicken collapsin or its homolog human Sema III (H-sema III), selectively induce extending axonal growth processes to collapse and/or turn away and, therefore, not establish connections with the secreting neuron (Fan J. et al, (1995), *Neuron* 14, 263). The net effect of this collapse is a chemorepulsion and redirection of the extending processes. In contrast, human CD100 is the only semaphorin identified that functions in the hematopoietic system, in particular in modulating a B cell response.

The structural similarities between CD100 and the semaphorin family of proteins indicate that CD100 plays a role in the nervous system in addition to its role in the immune system. CD100 agents of the invention can also be used for modulating communication or

- 11 -

interaction between a neuron and an immune cell, such as a neuron. As such, the CD100 antigens of the invention will be used in modulating nerve cell development and/or modulating the interaction between the immune and nervous system.

5 (c) Immunoglobulin-like domain

As defined in the art, an immunoglobulin-like domain has certain characteristics and encompasses two cysteines separated by about 60 amino acids and including up to about 20 amino acids flanking this region on either side. Human and murine CD100 have a first cysteine located at amino acid position 576 and a second cysteine located at amino acid
10 position 624 of amino acid sequences shown in Figure 1 (SEQ ID NO: 2) and in Figure 14 (SEQ ID NO: 9). Accordingly, a preferred immunoglobulin domain of CD100 corresponds to about amino acid 566 to about amino acid 630 of SEQ ID NO: 2 or SEQ ID NO: 9. However, additional flanking amino acids of amino acids 566-630 can also be included in the Ig-like domain. Accordingly, in one embodiment, the Ig-like domain of CD100
15 corresponds to about amino acids 554 to about amino acid 630. In another embodiment, an Ig-like domain can correspond to less than amino acids 566-630. These Ig-like domains are within the scope of the invention and are intended to be included in the term "CD100 Ig-like domain". A "CD100 Ig-like domain including amino acids 566-630 of SEQ ID NO: 2 or SEQ ID NO: 9" is also intended to include portions of CD100 which can be defined as
20 Ig-like domains.

(d) Stalk domain

The stalk domain of CD100 is defined as a region located between the Ig-like domain and a transmembrane region. This region is rich in charged amino acids and has
25 proteolytic enzyme recognition sites. Accordingly, the stalk domain corresponds to about amino acid 631 to about amino acid 733 of human CD100 (SEQ ID NO: 2) and to about amino acid 631 to about amino acid 732 of murine CD100 (SEQ ID NO: 9). The stalk domain can also include additional amino acid residues at the N-terminal end (e.g., residues which comprise the TM membrane). Alternatively, the stalk domain can include less
30 residues than amino acids 631 to 732 or 733. These stalk domains are intended to be included in the term "CD100 stalk domain". The term "CD100 stalk domain including amino acids 631-733 of human CD100 (SEQ ID NO: 2) or amino acids 631-732 of murine CD100 (SEQ ID NO: 9)" is also intended to include portions of CD100 which can be defined as stalk domains.

35 The stalk domain allows a membrane bound CD100 protein to become soluble CD100 protein by proteolytic cleavage in this domain. In fact, soluble CD100 protein has been observed in supernatant from cells transfected with a CD100 cDNA. Accordingly, the CD100 nucleic acid of the invention allows production of membrane bound as well a soluble CD100 protein. Accordingly, within the scope of the invention are soluble CD100

- 12 -

proteins which are produced by proteolytic cleavage at the stalk region. Such proteins have similar uses as membrane bound CD100. Within the scope of the invention are methods for increasing production of soluble CD100, comprising incubating cells having membrane bound CD100 with a protease capable of cleaving the protein at the stalk region. Proteases capable of cleaving CD100 at the stalk domain can be identified according to the amino acid sequence of the stalk domain and other methods known in the art. Furthermore, the nucleic acid encoding the stalk domain can be used to produce recombinant proteins, e.g., other than CD100 proteins which will be membrane bound, but will be able to be cleaved from the membrane. It may be preferable to include a CD100 transmembrane domain in the recombinant construct containing the CD100 stalk domain. Accordingly, the invention provides nucleic acids comprising the stalk domain and the transmembrane domain of a CD100 protein, for, e.g., production of recombinant proteins which will be partly membrane bound and partly in solution.

(e) Transmembrane domain

As defined in the art, a transmembrane domain is a hydrophobic region.

Accordingly, the transmembrane domain of human CD100 can be defined as a region from about amino acid 735 to about amino acid 753 of SEQ ID NO: 2 (Figures 1 and 2). The transmembrane domain of murine CD100 can be defined as a region from about amino acid 734 to about amino acid 752 of SEQ ID NO: 9. Also included in the term "CD100 transmembrane domain" are regions of CD100 corresponding essentially to amino acids 735-753 or 734-752, which lack one or more amino acids or which have one or more additional amino acids flanking this region and derived from the sequence of CD100.

Within the scope of the invention are nucleic acids encoding the transmembrane domain of CD100, which can be used to produce membrane bound recombinant proteins; e.g., proteins other than CD100. Accordingly, a nucleic acid encoding the transmembrane domain of CD100 can be genetically linked to a nucleic acid encoding a protein, such that the protein will be membrane bound.

(f) Cytoplasmic domain

The cytoplasmic domain of CD100 can be defined as the C-terminal portion of the protein following the transmembrane domain. Accordingly, a cytoplasmic domain of human CD100 is a portion of the protein from about amino acid 754 to about amino acid 862 of SEQ ID NO: 2. A cytoplasmic domain of murine CD100 is a portion of the protein from about amino acid 753 to about amino acid 261 of SEQ ID NO: 9.

A consensus site for tyrosine phosphorylation, KPALTGY (SEQ ID NO: 5) from amino acid 808 to amino acid 813 in the cytoplasmic tail of human CD100 and from amino acid 807 to amino acid 812 of murine CD100 supports the predicted association of CD100 with a tyrosine kinase (Sidorenko S., et al, "Identification of antigens associated with

- 13 -

protein kinases by activation antigens panel mAb." S. F. Schlossman, et al., Eds., *Leucocyte Typing V* (Oxford University Press, Oxford, 1995), vol. 1.; RuddC., et al., "Identification of antigens associated with protein kinases by activation antigen panel mAb." S. F. Schlossman, et al., Eds., *Leucocyte Typing V* (Oxford University Press, Oxford, 1995), vol. 1. Accordingly, the tyrosine residue of this tyrosine phosphorylation site can be phosphorylated.

The cytoplasmic domain of CD100 can be used, e.g., for identifying proteins or other molecules which interact with the cytoplasmic domain and which are, e.g., involved in signal transduction.

10 A CD100 molecule of the invention can thus be defined as comprising a signal sequence of about 21 or 23 amino acids (about amino acids 1-21 or about amino acids 1-23 of the sequence shown in Figure 2 (SEQ ID NO: 2) or the sequence shown in Figure 14 (SEQ ID NO: 9)) followed by a semaphorin domain of about 512 amino acids (about amino acids 42-553 of the sequence shown in Figure 2 (SEQ ID NO: 2) or the sequence shown in Figure 14 (SEQ ID NO: 9)), an immunoglobulin-like (Ig-like) domain of about 65 amino acids (about amino acids 566-630 of the sequence shown in Figure 2 (SEQ ID NO: 2) or the sequence shown in Figure 14 (SEQ ID NO: 9)), a lysine-rich stretch of 104 amino acids, a stalk domain of about 103 or 104 amino acids (about amino acids 631-734 of the sequence shown in Figure 2 (SEQ ID NO: 2) or amino acids 631-733 of the sequence shown in Figure 14 (SEQ ID NO: 9)), a hydrophobic transmembrane region of about 19 amino acids (about amino acids 735-753 of the sequence shown in Figure 2 (SEQ ID NO: 2) or about amino acids 734-752 of the sequence shown in Figure 14 (SEQ ID NO: 9)), and a cytoplasmic tail of about 109 amino acids (about amino acids 754-862 of the sequence shown in Figure 2 (SEQ ID NO: 2) or about amino acids 753-861 of the sequence shown in Figure 14 (SEQ ID NO: 9)).

Accordingly, this invention pertains to CD100 molecules (e.g., antigens, proteins) and to active portions thereof, such as peptides having an activity of CD100. The phrases "an activity of CD100" or "having a CD100 activity" are used interchangeably herein to refer to molecules such as proteins and peptides which are capable of stimulating a leukocyte response, such as a B cell response, e.g., B cell aggregation, and which preferably include a semaphorin domain or an active portion thereof. The phrase "active portion of a semaphorin domain" refers to those portions of a semaphorin domain that are required to mediate, alone, or in collaboration with other portions of the protein, a CD100 activity. Preferred molecules having a CD100 activity are those which are capable of stimulating B cell differentiation. Other preferred molecules having a CD100 activity are capable of stimulating B cell viability, and/or reducing the expression of CD23. Molecules having a CD100 activity are also intended to include molecules which are capable of stimulating a T cell response, such as stimulating proliferation of T cells in the presence of a primary activation signal and which preferably include a semaphorin domain or active portion

- 14 -

thereof. Even more preferred molecules of the invention include CD100 antigens which are capable of stimulating a B cell response and a T cell response. Particularly preferred molecules within the scope of the invention include those which are structurally similar to human CD100, i.e., molecules which preferably comprise in addition to the sema domain, an immunoglobulin-like domain, a transmembrane domain, a cytoplasmic domain having a tyrosine phosphorylation site, or any combination of these domains.

Various aspects of the invention are described in further detail in the following subsections:

I. Isolated Nucleic acid Molecules

One aspect of this invention pertains to isolated nucleic acid molecules that encode a novel CD100 antigen, such as human CD100, fragments of such nucleic acids, or equivalents thereof. The term "nucleic acid molecule" as used herein is intended to include such fragments or equivalents and refers to DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA). The nucleic acid molecule may be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, may be free of other cellular material.

The term "equivalent" is intended to include nucleotide sequences encoding functionally equivalent CD100 antigens or functionally equivalent peptides having a CD100 activity. Functionally equivalent CD100 antigens or peptides is intended to include antigens which are capable of stimulating a leukocyte response, such as a B cell response, e.g., B cell aggregation and preferably contain a semaphorin domain or an active portion thereof. Functionally equivalent CD100 antigens are also preferably capable of stimulating B cell differentiation, prolonging B cell viability, and/or decreasing CD23 expression. Functionally equivalent CD100 antigens or peptides also include antigens which are capable of providing a costimulatory signal to T cells and preferably contain a semaphorin domain or an active portion thereof. Preferred functionally equivalent CD100 antigens include antigens which are capable of stimulating a B cell response and a T cell response, and which preferably comprise a semaphorin domain or active portion thereof.

Other equivalents of CD100 antigens include structural equivalents. Structural equivalents of a CD100 antigen preferably comprise a semaphorin domain or portion thereof, an Ig-like domain or portion thereof, a transmembrane domain or portion thereof, and/or a cytoplasmic domain or portion thereof. A portion of a CD100 antigen is at least about 20 amino acid residues in length, more preferably at least about 40 amino acid residues in length, and even more preferably at least about 60 amino acid residues in length.

- 15 -

Preferred nucleic acids of the invention include nucleic acid molecules comprising a nucleotide sequence provided in Figure 1 (SEQ ID NO: 1) or Figure 12 (SEQ ID NO: 8), fragments thereof or equivalents thereof.

In one embodiment, the invention pertains to a nucleic acid molecule which is a naturally occurring form of a nucleic acid molecule encoding a CD100 antigen, such as a CD100 antigen having an amino acid sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). Preferably, a naturally occurring form of a nucleic acid encoding CD100 is derived from hematopoietic cells, such as activated lymphocytes. Such naturally occurring equivalents can be obtained, for example, by screening a cDNA library, prepared with RNA from hematopoietic cells, with a nucleic acid molecule having a sequence shown in Figure 1 (SEQ ID NO: 1) or in Figure 12 (SEQ ID NO: 8) under high stringency hybridization conditions. Such conditions are further described herein.

Also within the scope of the invention are nucleic acids encoding natural variants and isoforms of CD100 antigens, such as splice forms. Northern blot hybridization of a CD100 cDNA to RNA from lymphocytes and non-hematopoietic tissues indicated the existence of several mRNA hybridizing to CD100 DNA (Example 2). Such natural variants are within the scope of the invention. Furthermore, it is likely that secreted isoforms of CD100 exist, since CD100 is related to proteins from the semaphorin family, which are either secreted or membrane bound proteins. Such naturally secreted forms of CD100 are also within the scope of the invention.

In a preferred embodiment, the nucleic acid molecule encoding a CD100 antigen is a cDNA. Preferably, the nucleic acid molecule is a cDNA molecule consisting of at least a portion of a nucleotide sequence encoding human CD100, as shown in Figure 1 (SEQ ID NO: 1). A preferred portion of the cDNA molecule of Figure 1 (SEQ ID NO: 1) includes the coding region of the molecule (SEQ ID NO: 22). Other preferred portions include those which code for domains of CD100, such as the extracellular domain, the semaphorin domain, the immunoglobulin domain, the transmembrane domain, the cytoplasmic domain, or any combination thereof.

In another embodiment, the nucleic acid of the invention encodes a CD100 antigen or active fragment thereof having an amino acid sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). In yet other embodiment, preferred nucleic acid molecules encode a peptide having an overall amino acid sequence identity or similarity of at least about 50%, more preferably at least about 60%, more preferably at least about 70%, more preferably at least about 80%, more preferably 86% and most preferably at least about 90% with an amino acid sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). Preferred nucleic acids within the scope of the invention include nucleic acids encoding a protein or peptide having an overall similarity of at least about 91% with an amino acid sequence SEQ ID NO: 2. Nucleic acids which encode peptides having an overall amino acid sequence identity or similarity of at least about 93%, more preferably at

- 16 -

least about 95%, and most preferably at least about 98-99% with a sequence set forth in Figure 2 (SEQ ID NO: 2) are also within the scope of the invention. Homology, also termed herein "identity" refers to sequence similarity between two protein (peptides) or between two nucleic acid molecules. Homology can be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequences is occupied by the same nucleotide base or amino acid, then the molecules are homologous, or identical, at that position. A degree (or percentage) of homology between sequences is a function of the number of matching or homologous positions shared by the sequences. When a position in the compared amino acid sequences is occupied by an amino acid of a similar type, i.e., a conserved amino acid (see definition herein) then the molecules are similar in that position. A degree of similarity between amino acid sequences is defined as the proportion of the sum of the number of identical and conserved amino acid, and the total number of amino acids.

Isolated nucleic acids encoding a peptide having a CD100 activity, as described herein, and having a sequence which differs from nucleotide sequence shown in Figure 1 (SEQ ID NO: 1) or Figure 12 (SEQ ID NO: 8) due to degeneracy in the genetic code are also within the scope of the invention. Such nucleic acids encode functionally equivalent peptides (e.g., having a CD100 activity) or structurally equivalent peptides but differ in sequence from the sequence of Figure 2 (SEQ ID NO: 2) or Figure 14 (SEQ ID NO: 9) due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and CAC are synonyms for histidine) may occur due to degeneracy in the genetic code. As one example, DNA sequence polymorphisms within the nucleotide sequence of a CD100 antigen (especially those within the third base of a codon) may result in "silent" mutations in the DNA which do not affect the amino acid encoded. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the CD100 antigen will exist within a population. It will be appreciated by one skilled in the art that these variations in one or more nucleotides (up to about 3-4% of the nucleotides) of the nucleic acids encoding peptides having the activity of a CD100 antigen may exist among individuals within a population due to natural allelic variation. Any and all such nucleotide variations and resulting amino acid polymorphisms are within the scope of the invention. Furthermore, there may be one or more isoforms or related, cross-reacting family members of the CD100 antigen described herein. Such isoforms or family members are defined as proteins related in function and amino acid sequence to a CD100 antigen, but encoded by genes at different loci. Such isoforms or family members are within the scope of the invention.

A "fragment" of a nucleic acid encoding a CD100 antigen is defined as a nucleotide sequence having fewer nucleotides than the nucleotide sequence encoding the entire amino acid sequence of a CD100 antigen, such as human CD100. A fragment of a nucleic acid is

- 17 -

at least about 20 nucleotides, preferably at least about 30 nucleotides, more preferably at least about 40 nucleotides, even more preferably at least about 50 nucleotides long. Also within the scope of the invention are nucleic acid fragments which are at least about 60, 70, 80, 90, 100 or more nucleotides long. Preferred fragments include fragments which encode a peptide having a CD100 activity (i.e., the ability to stimulate a leukocyte response, such as a B cell response, e.g., B cell aggregation, or a T cell response, e.g., T cell proliferation in the presence of a primary activation signal and which preferably contain a sema domain or an active portion thereof). Thus, a preferred peptide having a CD100 activity has a sema domain or active portion thereof, and stimulates aggregation of B cells. Another preferred peptide having CD100 activity has a sema domain or active portion thereof and provides a costimulatory signal to T cells. For determining whether a fragment of a CD100 antigen, such as a fragment of human CD100 is capable of inducing a B cell response, such as B cell aggregation, the peptide, either in soluble form or membrane bound is added to a culture of B cells. Aggregation of B cells can then be visualized macroscopically or under a microscope. Preferred conditions for a B cell aggregation assay are described in the Example section. Assays for determining whether a fragment of a CD100 antigen is capable of providing a costimulatory signal to T cells the following assay can be performed. T cells, such as CD4+ T cells, are incubated in the presence of a primary activation signal, such as an anti-CD3 antibody and various amounts of a CD100 fragment, e.g., expressed on the surface of cells. Following incubation for about 3 days, a proliferation assay is performed, which is indicative of the proliferation rate of the T cells. Thus, a fragment of a CD100 antigen which is capable of costimulating T cells is a fragment of a CD100 antigen which in the presence of a primary T cell activation signal stimulates the T cells to proliferate at a rate that is greater than proliferation rate of T cells contacted only with a primary activation signal. Proliferation assays can also be performed as described in the PCT Application No. PCT/US94/08423.

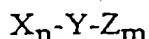
The fragments of a CD100 antigen, such as human CD100, are also preferably capable of stimulating B cell differentiation. For example, a CD100 fragment of the invention can stimulate the differentiation of B cells from a lymphoblast to a centrocyte. Other CD100 fragments of the invention stimulate the differentiation of B cells into antibody secreting plasma cells or memory B cells. It is also possible that the same fragment will stimulate differentiation of B cells into either memory B cells or antibody secreting B cells depending on the conditions of stimulation. Increased B cell differentiation can be shown, for example, by comparing the expression of B cell markers on B cells incubated in the presence or absence of the CD100 protein fragments. B cells at specific stages of differentiation are characterized by the expression of specific membrane proteins. For example, CD23, CD38, and CD40 are expressed on activated B cells. However, centrocytes and plasma cells lose membrane expression of CD23, CD38 and immunoglobulin molecules, such as IgM and IgD. A plasma cell can also be identified by

- 18 -

its secretion of antibody. Thus, the ability of a peptide of the invention to induce B cell differentiation can be shown by measuring surface levels of specific B cell markers.

Preferred fragments of the invention are capable of reducing the level of expression of CD23 induced by CD40 crosslinking. This can be demonstrated, for example, by CD23 fluorescence staining and flow cytometry analysis of B cells stimulated through CD40 and incubated in the presence or absence of CD100 fragments. Methods that can be used for showing the biological activities of CD100 on B cells are further described in the Example section.

Other preferred nucleic acid fragments encode peptides comprising at least part of one or more specific domains of a CD100 antigen. Preferred nucleic acid fragments encode peptides of at least about 20 amino acid residues in length, preferably at least about 40 amino acid residues and length, and more preferably at least about 60 amino acid residues in length. Nucleic acid fragments which encode peptides of at least about 80 amino acid residues in length, at least about 100 amino acid residues in length, at least about 200 amino acid residues in length, at least about 300 amino acid residues in length, at least about 400 amino acid residues in length, at least about 500 amino acid residues in length, or more amino acids in length are also within the scope of the invention. Particularly preferred nucleic acid fragments encode a peptide having an amino acid sequence represented by a formula:



In the formula, Y comprises the semaphorin domain. Y is preferably a peptide having about amino acid residues 42-553 of the sequence shown in Figure 2 (SEQ ID NO: 2). Y can also be a peptide having about amino acid residues 42-553 of the sequence shown in Figure 14 (SEQ ID NO: 9). X_n and Z_m are additional amino acid residue(s) linked to Y by an amide bond. X_n and Z_m are selected from amino acid residues contiguous to Y in the amino acid sequence shown in Figure 2 (SEQ ID NO: 2) or Figure 14 (SEQ ID NO: 9). In the formula, X_n is amino acid residue(s) selected from amino acids contiguous to the amino terminus of Y in the sequence shown in Figure 2 (SEQ ID NO: 2) or Figure 14 (SEQ ID NO: 9), i.e., from amino acid residue 41 to 1. Z_m is amino acid residue(s) selected from amino acids contiguous to the carboxy terminus of Y in the sequence shown in Figure 2 (SEQ ID NO: 2) or Figure 14 (SEQ ID NO: 9), i.e., from amino acid residue 554 to 862. In addition, in the formula, n is a number from 0 to 41 ($n=0-41$) and m is a number from 0 to 310 ($m=0-310$). A particularly preferred peptide has an amino acid sequence represented by the formula X_n-Y-Z_m as above, where $n=0$ and $m=0$.

Particularly preferred nucleic acid fragments encode a peptide having an amino acid sequence represented by a formula X_n-Y-Z_m , wherein Y is selected from the group consisting of: an extracellular domain, which is preferably about amino acid residues 22-

- 19 -

630, amino acid residues 24-630, amino acid residues 22-734, or amino acid residues 24-734 of the sequence shown in Figure 2 (SEQ ID NO: 2) or amino acid residues 22-630, amino acid residues 24-630, amino acid residues 22-733, or amino acid residues 24-733 of the sequence shown in Figure 14 (SEQ ID NO: 9); an extracellular domain comprising the signal peptide, which is preferably about amino acid residues 1-630 or 1-734 of the sequence shown in Figure 2 (SEQ ID NO: 2) or amino acid residues 1-630 or 1-733 of the sequence shown in Figure 14 (SEQ ID NO: 9); an Ig-like domain, which is preferably about amino acid residues 566-630 or 554-630 of the sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9); a transmembrane domain, which is about amino acid residues 735-753 of the sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9); and a cytoplasmic domain, which is about amino acid residues 754-862 of the sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). In the formula, X_n and Z_m are additional amino acid residues linked to Y by an amide bond. X_n and Z_m are amino acid residues selected from amino acids contiguous to Y in the amino acid sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). X_n is amino acid residues selected from amino acids contiguous to the amino terminus of Y in the sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). Z_m is amino acid residues selected from amino acids contiguous to the carboxy terminus of Y in the sequence shown in Figure 2 (SEQ ID NO: 2) or in Figure 14 (SEQ ID NO: 9). According to the formula, n is a number from 0 to 753 (n=0-753) and m is a number from 0 to 234 (m=0-234). A particularly preferred peptide has an amino acid sequence represented by the formula X_n -Y- Z_m , where n=0 and m=0.

Nucleic acids of the invention also include nucleic acids encoding peptides having a formula X_n -Y- Z_m , wherein Y is a portion of any of the domains described above and X_n and Z_m are amino acids flanking Y.

Also within the scope of the invention are nucleic acids encoding a signal domain having at least about 68% identity with a signal domain of SEQ ID NO: 2 or SEQ ID NO: 9, nucleic acids encoding a sema domain having at least about 88% identity with a sema domain of SEQ ID NO: 2 or SEQ ID NO: 9, nucleic acids encoding an Ig-like domain having at least about 84% identity with an Ig-like domain of SEQ ID NO: 2 or SEQ ID NO: 9, nucleic acids encoding a stalk domain having at least about 70% identity with a stalk domain of SEQ ID NO: 2 or SEQ ID NO: 9, nucleic acids encoding a transmembrane domain having at least about 84% identity with a transmembrane domain of SEQ ID NO: 2 or SEQ ID NO: 9, and nucleic acids encoding a cytoplasmic domain having at least about 94% identity with a cytoplasmic domain of SEQ ID NO: 2 or SEQ ID NO: 9. Proteins encoded by the above-described nucleic acids are also within the scope of the invention.

Other nucleic acids within the scope of the invention include nucleic acids encoding a peptide having the formula X_n -Y- Z_m , wherein Y comprises an amino acid sequence that is at least about 50%, preferably at least about 60%, more preferably at least about 70%,

- 20 -

more preferably at least about 80%, more preferably at least about 90%, and most preferably at least about 95% identical in amino acid sequence with an amino acid sequence of the semaphorin domain, the extracellular domain, the Ig-like domain, or the cytoplasmic domain shown in Figure 2 (SEQ ID NO: 2). In yet other embodiment, the amino acid sequence represented by X_n and Z_m are at least about 50%, preferably at least about 60%, more preferably at least about 70%, more preferably at least about 80%, more preferably at least about 90%, and most preferably at least about 95% identical in amino acid sequence with an amino acid sequence shown in Figure 2, SEQ ID NO: 2.

Yet other preferred nucleic acids of the invention comprise several nucleic acids defined above. Thus, within the scope of the invention are nucleic acids encoding a peptide having a formula X_n -Y- Z_m , wherein Y comprises a semaphorin domain and a peptide having the same formula, wherein Y comprises an Ig-like domain. Further within the scope of the invention are nucleic acids encoding a peptide having a formula X_n -Y- Z_m , wherein Y comprises a semaphorin domain and a peptide having the same formula, wherein Y comprises a transmembrane domain.

The invention also pertains to nucleic acid molecules comprising a nucleic acid encoding a semaphorin domain, or an active portion thereof, that is at least about 60%, preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90%, even more preferably at least about 95%, and most preferably at least about 98% identical in amino acid sequence with the semaphorin domain of human CD100 shown in Figure 2 (SEQ ID NO: 2). Preferred nucleic acids comprise an open reading frame having at least about 83% identity with an open reading frame of SEQ ID NO: 1. Also within the scope of the invention are nucleic acids comprising a first nucleic acid encoding a semaphorin domain, or an active portion thereof, which is at least about 50%, preferably at least about 60%, more preferably at least about 70%, even more preferably at least about 80%, and even more preferably at least about 90% identical in amino acid residues to the semaphorin domain of the human CD100 shown in Figure 2 (SEQ ID NO: 2) and a second nucleic acid encoding an Ig-like domain, which is at least about 40%, preferably at least about 50%, more preferably at least about 60%, more preferably at least about 70%, more preferably at least about 80%, and most preferably at least about 90% identical in amino acid sequence with the Ig-like domain of the human CD100 shown in Figure 2 (SEQ ID NO: 2). Even more preferred nucleic acids comprise a third nucleic acid encoding a cytoplasmic domain, which is at least about 40%, preferably at least about 50%, more preferably at least about 60%, more preferably at least about 70%, more preferably at least about 80%, and most preferably at least about 90% identical in amino acid sequence with a cytoplasmic domain of the human CD100 shown in Figure 2 (SEQ ID NO: 2).

Nucleic acid fragments within the scope of the invention include those capable of hybridizing with nucleic acids from other animal species for use in screening protocols to detect novel proteins that are related to the CD100 antigen described herein. These and

- 21 -

other fragments are described in detail herein. Generally, the nucleic acid encoding a fragment of a CD100 antigen will be selected from the bases coding for the mature protein, however, in some instances it may be desirable to select all or part of a fragment or fragments from the leader or signal sequence or non-coding portion of a nucleotide sequence. Preferred nucleic acid fragments for detecting and/or isolating nucleic acids encoding a CD100 antigen comprise any portion of the coding sequence of CD100 excluding the semaphorin domain. In other embodiments, it may be desirable to select a nucleic acid encoding the semaphorin domain. Nucleic acids within the scope of the invention may also contain linker sequences, modified restriction endonuclease sites and other sequences useful for molecular cloning, expression or purification of recombinant protein or fragments thereof. These and other modifications of nucleic acid sequences are described in further detail herein.

A nucleic acid encoding a peptide having an activity of a CD100 activity, such as human CD100, can be obtained from mRNA present in activated B lymphocytes or activated T lymphocytes. Alternatively, a nucleic acid encoding a peptide having an activity of a CD100 antigen can be obtained from other cells and tissues, since CD100 mRNA was also observed in tissues such as skeletal muscle (Example 2). It should also be possible to obtain nucleic acid sequences encoding such CD100 antigens from genomic DNA. For example, the gene encoding the CD100 antigen can be cloned from either a cDNA or a genomic library in accordance with protocols herein described. A cDNA encoding a CD100 antigen can be obtained by isolating total mRNA from an appropriate cell line. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding CD100 antigens can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. A preferred nucleic acid is a cDNA encoding the human CD100 antigen having the sequence depicted in Figure 1 (SEQ ID NO: 1).

Another aspect of the invention provides a nucleic acid which hybridizes under high or low stringency conditions to a nucleic acid which encodes a peptide having all or a portion of an amino acid sequence shown in Figure 2 (SEQ ID NO: 2). Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 25 °C to a high stringency of about 0.2 X SSC at 65°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high

- 22 -

stringency conditions, at about 65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of Figure 1, SEQ ID NO: 1 corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural CD100.

A cDNA encoding mouse CD100 has been cloned by cross-hybridization according to the methods described in the previous paragraph (Example 8). Accordingly, other nucleic acids can be obtained by similar methods.

In addition to naturally-occurring allelic variants of the CD100 sequence that may exist in the population, the skilled artisan will further appreciate that changes may be introduced by mutation into the nucleotide sequence of Figure 1, SEQ ID NO: 1 or Figure 12 (SEQ ID NO: 8), thereby leading to changes in the amino acid sequence of the encoded CD100 protein, without altering the functional ability of the CD100 protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues may be made in the sequence of Figure 1, SEQ ID NO: 1. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of CD100 (e.g., the sequence of Figure 2, SEQ ID NO: 2) without altering the ability of CD100 to stimulate a leukocyte response, such as a B cell response, i.e., B cell aggregation, whereas an "essential" amino acid residue is required for such activity. For example, amino acid residues of CD100 that are strongly conserved within members of a semaphorin family are predicted to be essential to CD100 activity and thus are not likely to be amenable to alteration.

An isolated nucleic acid molecule encoding a CD100 protein homologous to the protein of Figure 2, SEQ ID NO: 2 can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of Figure 1, SEQ ID NO: 1 such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into Figure 1, SEQ ID NO: 1 by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art, including basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in CD100 is preferably replaced with

- 23 -

another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a CD100 coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for or CD100 activity to identify mutants that retain CD100 activity. Following mutagenesis of a nucleic acid having a sequence shown in Figure 1, SEQ ID NO: 1, the encoded protein can be expressed recombinantly and activity of the protein can be determined. A suitable assay for testing the activity of a CD100 protein or active portion thereof and mutated CD100 proteins is described in further detail herein.

In addition to the nucleic acid molecules encoding CD100 proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid.

The antisense nucleic acid can be complementary to an entire CD100 coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding CD100. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (e.g., the entire coding region of Figure 1, SEQ ID NO: 1). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding CD100. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding CD100 disclosed herein (e.g., Figure 1, SEQ ID NO: 1), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule may be complementary to the entire coding region of CD100 mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of CD100 mRNA. For example, the antisense oligonucleotide may be complementary to the region surrounding the translation start site of CD100 mRNA. An antisense oligonucleotide can be, for example, about 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense

- 24 -

nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

5 In another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. A ribozyme having specificity for a CD100-encoding nucleic acid can be designed based upon the nucleotide sequence of a CD100 cDNA disclosed herein
10 (i.e., SEQ ID NO: 1). See for example Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742. Alternatively, CD100 mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See for example Bartel, D. and Szostak, J.W. (1993) *Science* 261: 1411-1418.

The nucleic acid sequences of the invention can also be chemically synthesized
15 using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

20

II. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding CD100 (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting
25 another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial
30 vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression
35 vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors,

- 25 -

such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means
5 that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence
10 (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990).
15 Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector may depend on such factors as the choice of the host cell to be transformed, the level of expression of
20 protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., CD100 proteins, mutant forms of CD100, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression
25 of CD100 in prokaryotic or eukaryotic cells. For example, CD100 can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector may be transcribed and translated *in vitro*,
30 for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion
35 vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from

- 26 -

the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nuc. Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the CD100 expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari. *et al.*, (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA).

Alternatively, CD100 can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al.*, (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow, V.A., and Summers, M.D., (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B., (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987), *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40.

- 27 -

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert et al. (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji et al. (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddell (1989) *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund et al. (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

In one embodiment, a recombinant expression vector containing DNA encoding a CD100 fusion protein is produced. A CD100 fusion protein can be produced by recombinant expression of a nucleotide sequence encoding a first peptide having a CD100 activity and a nucleotide sequence encoding a second peptide corresponding to a moiety that alters a characteristic of the first peptide, e.g., its solubility, affinity, stability or valency, for example, an immunoglobulin constant region. Preferably, the first peptide consists of a portion of the extracellular domain of a CD100 antigen, such as the human CD100 antigen (e.g., approximately amino acid residues 22-734 of the sequence shown in Figure 2 (SEQ ID NO: 2)) or a semaphorin domain of a CD100 antigen, such as human CD100 (e.g., approximately amino acid residues 42-553 of the sequence shown in Figure 2 (SEQ ID NO: 2)). Preferred nucleic acids encoding a CD100Ig fusion protein comprise a nucleic acid encoding a peptide from the group of peptides having about amino acid residues 1-553, about amino acid residues 22-553, about amino acid residues 1-630, and about amino acid residues 22-630 of human CD100 shown in Figure 2 (SEQ ID NO: 2). The second peptide can include an immunoglobulin constant region, for example, a human C1 domain or C4 domain (e.g., the hinge, CH2 and CH3 regions of human IgC1, or human IgC4, see e.g., Capon et al. US 5,116,964, incorporated herein by reference). The immunoglobulin constant region may contain genetic modifications which reduce or eliminate effector activity inherent in the immunoglobulin structure. For example, DNA encoding the extracellular portion of human CD100 can be joined to DNA encoding the hinge, CH2 and CH3 regions of human IgC1 and/or IgC4 modified by site directed mutagenesis. A resulting CD100Ig fusion protein may have altered CD100 solubility, binding affinity, stability and/or valency (i.e., the number of binding sites available per molecule) and may

- 28 -

increase the efficiency of protein purification. Fusion proteins and peptides produced by recombinant techniques may be secreted and isolated from a mixture of cells and medium containing the protein or peptide. Alternatively, the protein or peptide may be retained cytoplasmically and the cells harvested, lysed and the protein isolated. A cell culture typically includes host cells, media and other byproducts. Suitable mediums for cell culture are well known in the art. Protein and peptides can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins and peptides. Techniques for transfecting host cells and purifying proteins and peptides are described in further detail herein.

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to CD100 RNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. et al., *Antisense RNA as a molecular tool for genetic analysis, Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to recombinant host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell may be any prokaryotic or eukaryotic cell. For example, CD100 protein may be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium

- 29 -

chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd Edition, Cold Spring Harbor Laboratory press (1989)), and other laboratory manuals.

5 For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable
10 markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker may be introduced into a host cell on the same vector as that encoding CD100 or may be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other
15 cells die).

Transfected cells which express peptides having a CD100 activity on the surface of the cell are also within the scope of this invention. In one embodiment, a host cell such as a COS cell is transfected with an expression vector directing the expression of a peptide having a CD100 activity on the surface of the cell. Such a transfected host cell can be used
20 in methods for identifying molecules which inhibit binding of CD100 to its receptor or ligand on, e.g., B cells or which interfere with intracellular signaling in response to CD100 interaction. Such cells can also be used for stimulating B cell aggregation and/or B cell differentiation and/or T cell proliferation according to the methods of the invention. In another embodiment, a tumor cell such as a sarcoma, a melanoma, a leukemia, a
25 lymphoma, a carcinoma or a neuroblastoma is transfected with an expression vector directing the expression of at least one peptide having a CD100 activity on the surface of the tumor cell. In some instances, it may be beneficial to transfect a tumor cell to coexpress other molecules, including a CD40 ligand, major histocompatibility complex (MHC) proteins, for example MHC class II and chain proteins or an MHC class I chain protein, and, if necessary, a β_2 microglobulin protein. Such transfected tumor cells can be used to
30 induce tumor immunity in a subject.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) CD100 protein. Accordingly, the invention further provides methods for producing CD100 protein using the host cells of the invention. In one
35 embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding CD100 has been introduced) in a suitable medium until CD100 is produced. In another embodiment, the method further comprises isolating CD100 from the medium or the host cell.

- 30 -

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which CD100-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which
5 exogenous CD100 sequences have been introduced into their genome or homologous recombinant animals in which endogenous CD100 sequences have been altered. Such animals are useful for studying the function and/or activity of CD100 and for identifying and/or evaluating modulators of CD100 activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which one or more
10 of the cells of the animal includes a transgene. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more
15 preferably a mouse, in which an endogenous CD100 gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing CD100-
20 encoding nucleic acid into the male pronuclei of a fertilized oocyte, e.g., by microinjection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human CD100 cDNA sequence of Figure 1, SEQ ID NO: 1 or the murine cDNA sequence shown in Figure 12, SEQ ID NO: 8 can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human CD100 gene, such as a
25 mouse CD100 gene, can be isolated based on hybridization to the human CD100 cDNA (described further in subsection I above) and used as a transgene. Such a mouse cDNA has been isolated (see Example 8 herein). Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the CD100 transgene to
30 direct expression of CD100 protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, both by Leder et al., U.S. Patent No. 4,873,191 by Wagner et al. and in Hogan, B., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press,
35 Cold Spring Harbor, N.Y., 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the CD100 transgene in its genome and/or expression of CD100 mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional

- 31 -

animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding CD100 can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a CD100 gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the CD100 gene. The CD100 gene may be a human gene (e.g., from a human genomic clone isolated from a human genomic library screened with the cDNA of Figure 1, SEQ ID NO: 1), but more preferably, is a non-human homologue of a human CD100 gene. For example, a mouse CD100 gene can be isolated from a mouse genomic DNA library using the human CD100 cDNA of Figure 1, SEQ ID NO: 1 or preferably the murine cDNA of Figure 12, SEQ ID NO: 8 as a probe. The mouse CD100 gene then can be used to construct a homologous recombination vector suitable for altering an endogenous CD100 gene in the mouse genome. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous CD100 gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous CD100 gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous CD100 protein). In the homologous recombination vector, the altered portion of the CD100 gene is flanked at its 5' and 3' ends by additional nucleic acid of the CD100 gene to allow for homologous recombination to occur between the exogenous CD100 gene carried by the vector and an endogenous CD100 gene in an embryonic stem cell. The additional flanking CD100 nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see e.g., Thomas, K.R. and Capecchi, M. R. (1987) *Cell* 51:503 for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced CD100 gene has homologously recombined with the endogenous CD100 gene are selected (see e.g., Li, E. et al. (1992) *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras (see e.g., Bradley, A. in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E.J. Robertson, ed. (IRL, Oxford, 1987) pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, A. (1991) *Current Opinion in Biotechnology* 2:823-829 and in PCT International

- 32 -

Publication Nos.: WO 90/11354 by Le Mouellec et al.; WO 91/01140 by Smithies et al.; WO 92/0968 by Zijlstra et al.; and WO 93/04169 by Berns et al.

III. Isolated CD100 Proteins and Anti-CD100 Antibodies

Another aspect of the invention pertains to isolated CD100 proteins and active fragments thereof, i.e, peptides having a CD100 activity, such as human CD100. This invention also provides a preparation of CD100 or fragment thereof. An "isolated" protein is substantially free of cellular material or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized.

In a preferred embodiment, the CD100 protein has an amino acid sequence shown in Figure 2, SEQ ID NO: 2. In other embodiments, the CD100 protein is substantially homologous or similar to Figure 2, SEQ ID NO: 2 and retains the functional activity of the protein of Figure 2, SEQ ID NO: 2 yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the CD100 protein is a protein which comprises an amino acid sequence at least 80 % overall amino acid sequence identity with the amino acid sequence of Figure 2, SEQ ID NO: 2. Preferably, the protein is at least 90 % identical to a protein having an amino acid sequence shown in Figure 2, SEQ ID NO: 2 or in Figure 14, SEQ ID NO: 9, more preferably at least 95 % identical to a protein having an amino acid sequence shown in Figure 2, SEQ ID NO: 2 or in Figure 14, SEQ ID NO: 9, even more preferably at least 98-99 % identical to a protein having an amino acid sequence shown in Figure 2, SEQ ID NO: 2 or in Figure 14, SEQ ID NO: 9.

An isolated CD100 protein may comprise the entire amino acid sequence of Figure 2, SEQ ID NO: 2 or a biologically active portion thereof. For example, an active portion of CD100 can comprise a mature form of CD100 in which a hydrophobic, amino-terminal signal sequence is absent. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for a CD100 activity as described in detail above. For example, a peptide having a CD100 activity may differ in amino acid sequence from the human CD100 depicted in Figure 2 (SEQ ID NO: 2), but such differences result in a peptide which functions in the same or similar manner as CD100. Thus, peptides having the ability to stimulate a leukocyte response, such as a B cell response, e.g., B cell aggregation, and which preferably has a semaphorin domain or an active portion thereof are within the scope of the invention. Preferred peptides of the invention include those which are further capable of inducing B cell differentiation, stimulating B cell survival, downregulating CD40 induced CD23 expression and/or costimulating T cell proliferation.

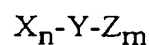
One embodiment provides a CD100 derived peptide having B cell binding activity, but lacking the ability to stimulate a leukocyte response, such as a B cell response. Such a peptide can be used to inhibit or block B cell differentiation or T cell proliferation in a

- 33 -

subject. Alternatively, a peptide having both B cell binding activity and the ability to deliver a stimulatory signal to B cells can be used to stimulate or enhance a B cell response, such as B cell aggregation and/or antibody production in a subject. Similarly, a peptide having T cell binding activity and the ability to deliver a stimulatory signal to T cells can be used to stimulate or enhance a T cell response, such as T cell proliferation. Various modifications of the CD100 protein to produce these and other functionally equivalent peptides are described in detail herein. The term "peptide" as used herein, refers to peptides, proteins and polypeptides.

A peptide can be produced by modification of the amino acid sequence of the human CD100 protein shown in Figure 2 (SEQ ID NO: 2) or murine CD100 protein shown in Figure 14 (SEQ ID NO: 9), such as a substitution, addition or deletion of an amino acid residue which is not directly involved in the function of CD100.

Peptides of the invention are typically at least about 30 amino acid residues in length, preferably at least about 40 amino acid residues in length, more preferably at least about 50 amino acid residues in length, and most preferably about 60 amino acid residues in length. Peptides having CD100 activity and including at least about 80 amino acid residues in length, at least about 100 amino acid residues in length, at least about 200, at least about 300, at least about 400, or at least about 500 or more amino acid residues in length are also within the scope of the invention. A preferred peptide includes an extracellular domain or portion thereof of the human CD100 antigen (e.g., about amino acid residues 22-734 or 24-734 of the sequence shown in Figure 2 (SEQ ID NO: 2). Other preferred peptides have an amino acid sequence represented by a formula:



where Y is selected from the group consisting of: an extracellular domain comprising the signal peptide, which is preferably about amino acid residues 1-630 or 1-734 of the sequence shown in Figure 2 (SEQ ID NO: 2); a semaphorin domain, which is preferably about amino acid residues 42-553 of the sequence shown in Figure 2 (SEQ ID NO: 2); an Ig-like domain, which is preferably about amino acid residues 566-630 or 554-630 of the sequence shown in Figure 2 (SEQ ID NO: 2); a transmembrane domain, which is about amino acid residues 735-753 of the sequence shown in Figure 2 (SEQ ID NO: 2); and a cytoplasmic domain, which is about amino acid residues 754-862 of the sequence shown in Figure 2 (SEQ ID NO: 2). In the formula, X_n and Z_m are additional amino acid residues linked to Y by an amide bond. X_n and Z_m are amino acid residues selected from amino acids contiguous to Y in the amino acid sequence shown in Figure 2 (SEQ ID NO: 2). X_n is amino acid residues selected from amino acids contiguous to the amino terminus of Y in the sequence shown in Figure 2 (SEQ ID NO: 2). Z_m is amino acid residues selected from amino acids contiguous to the carboxy terminus of Y in the sequence shown in Figure 2

- 34 -

(SEQ ID NO: 2). According to the formula, n is a number from 0 to 753 ($n=0-753$) and m is a number from 0 to 234 ($m=0-234$). A particularly preferred peptide has an amino acid sequence represented by the formula X_n-Y-Z_m , where $n=0$ and $m=0$.

Other peptides within the scope of the invention include those encoded by the nucleic acids described herein.

Another embodiment of the invention provides a substantially pure preparation of a peptide having a CD100 activity. Such a preparation is substantially free of proteins and peptides with which the peptide naturally occurs in a cell or with which it naturally occurs when secreted by a cell.

The term "isolated" as used throughout this application refers to a nucleic acid, protein or peptide having an activity of a CD100 antigen substantially free of cellular material or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. An isolated nucleic acid is also free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the organism from which the nucleic acid is derived.

The peptides and fusion proteins produced from the nucleic acid molecules of the present invention can also be used to produce antibodies specifically reactive with CD100 antigens. For example, by using a full-length CD100 antigen, such as an antigen having an amino acid sequence shown in Figure 2 (SEQ ID NO: 2), or a peptide fragment thereof, anti-protein/anti-peptide polyclonal antisera or monoclonal antibodies can be made using standard methods. A mammal, (e.g., a mouse, hamster, or rabbit) can be immunized with an immunogenic form of the protein or peptide which elicits an antibody response in the mammal. The immunogen can be, for example, a recombinant CD100 protein, or fragment thereof, a synthetic peptide fragment or a cell that expresses a CD100 antigen on its surface. The cell can be for example, a splenic B cell or a cell transfected with a nucleic acid encoding a CD100 antigen of the invention (e.g., a /CD100 cDNA) such that the CD100 antigen is expressed on the cell surface. The immunogen can be modified to increase its immunogenicity. For example, techniques for conferring immunogenicity on a peptide include conjugation to carriers or other techniques well known in the art. For example, the peptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassay can be used with the immunogen as antigen to assess the levels of antibodies.

Following immunization, antisera can be obtained and, if desired, polyclonal antibodies isolated from the sera. To produce monoclonal antibodies, antibody producing cells (lymphocytes) can be harvested from an immunized animal and fused with myeloma cells by standard somatic cell fusion procedures thus immortalizing these cells and yielding hybridoma cells. Such techniques are well known in the art. For example, the hybridoma technique originally developed by Kohler and Milstein (*Nature* (1975) 256:495-497) as well as other techniques such as the human B-cell hybridoma technique (Kozbar et al.,

- 35 -

Immunol. Today (1983) 4:72), the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al. *Monoclonal Antibodies in Cancer Therapy* (1985) Allen R. Bliss, Inc., pages 77-96), and screening of combinatorial antibody libraries (Huse et al., *Science* (1989) 246:1275). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with the peptide and monoclonal antibodies isolated.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with a peptide having the activity of a novel B lymphocyte antigen or fusion protein as described herein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the present invention is further intended to include bispecific and chimeric molecules having an anti-CD100 antigen (i.e., CD100) portion.

When antibodies produced in non-human subjects are used therapeutically in humans, they are recognized to varying degrees as foreign and an immune response may be generated in the patient. One approach for minimizing or eliminating this problem, which is preferable to general immunosuppression, is to produce chimeric antibody derivatives, i.e., antibody molecules that combine a non-human animal variable region and a human constant region. Chimeric antibody molecules can include, for example, the antigen binding domain from an antibody of a mouse, rat, or other species, with human constant regions. A variety of approaches for making chimeric antibodies have been described and can be used to make chimeric antibodies containing the immunoglobulin variable region which recognizes the gene product of the novel CD100 antigens of the invention. See, for example, Morrison et al., (1985), *Proc. Natl. Acad. Sci. U.S.A.* 81:6851 ; Takeda et al., (1985), *Nature* 314:452 , Cabilly et al., U.S. Patent No. 4,816,567; Boss et al., U.S. Patent No. 4,816,397; Tanaguchi et al., European Patent Publication EP171496; European Patent Publication 0173494, United Kingdom Patent GB 2177096B. It is expected that such chimeric antibodies would be less immunogenic in a human subject than the corresponding non-chimeric antibody.

For human therapeutic purposes, the monoclonal or chimeric antibodies specifically reactive with a CD100 antigen as described herein can be further humanized by producing human variable region chimeras, in which parts of the variable regions, especially the conserved framework regions of the antigen-binding domain, are of human origin and only the hypervariable regions are of non-human origin. General reviews of "humanized" chimeric antibodies are provided by Morrison, S. L. (1985) *Science* 229:1202-1207 and by Oi et al. (1986) *BioTechniques* 4:214. Such altered immunoglobulin molecules may be made by any of several techniques known in the art, (e.g., Teng et al., (1983), *Proc. Natl.*

- 36 -

Acad. Sci. U.S.A., 80:7308-7312; Kozbor et al., (1983), *Immunology Today*, 4:7279; Olsson et al., (1982), *Meth. Enzymol.*, 92:3-16), and are preferably made according to the teachings of PCT Publication WO92/06193 or EP 0239400. Humanized antibodies can be commercially produced by, for example, Scotgen Limited, 2 Holly Road, Twickenham, Middlesex, Great Britain. Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (see U.S. Patent 5,225,539 to Winter; Jones et al. (1986) *Nature* 321:552-525; Verhoeyan et al. (1988) *Science* 239:1534; and Beidler et al. (1988) *J. Immunol.* 141:4053-4060). Humanized antibodies which have reduced immunogenicity are preferred for immunotherapy in human subjects. Immunotherapy with a humanized antibody will likely reduce the necessity for any concomitant immunosuppression and may result in increased long term effectiveness for the treatment of chronic disease situations or situations requiring repeated antibody treatments.

As an alternative to humanizing a monoclonal antibody from a mouse or other species, a human monoclonal antibody directed against a human protein can be generated. Transgenic mice carrying human antibody repertoires have been created which can be immunized with a CD100 antigen, such as human CD100. Splenocytes from these immunized transgenic mice can then be used to create hybridomas that secrete human monoclonal antibodies specifically reactive with a CD100 antigen (see, e.g., Wood et al. PCT publication WO 91/00906, Kucherlapati et al. PCT publication WO 91/10741; Lonberg et al. PCT publication WO 92/03918; Kay et al. PCT publication 92/03917; Lonberg, N. et al. (1994) *Nature* 368:856-859; Green, L.L. et al. (1994) *Nature Genet.* 7:13-21; Morrison, S.L. et al. (1994) *Proc. Natl. Acad. Sci. USA* 81:6851-6855; Bruggeman et al. (1993) *Year Immunol* 7:33-40; Tuailon et al. (1993) *PNAS* 90:3720-3724; and Bruggeman et al. (1991) *Eur J Immunol* 21:1323-1326).

Monoclonal antibody compositions of the invention can also be produced by other methods well known to those skilled in the art of recombinant DNA technology. An alternative method, referred to as the "combinatorial antibody display" method, has been developed to identify and isolate antibody fragments having a particular antigen specificity, and can be utilized to produce monoclonal antibodies that bind a CD100 antigen of the invention (for descriptions of combinatorial antibody display see e.g., Sastry et al. (1989) *PNAS* 86:5728; Huse et al. (1989) *Science* 246:1275; and Orlandi et al. (1989) *PNAS* 86:3833). After immunizing an animal with a CD100 antigen, the antibody repertoire of the resulting B-cell pool is cloned. Methods are generally known for directly obtaining the DNA sequence of the variable regions of a diverse population of immunoglobulin molecules by using a mixture of oligomer primers and PCR. For instance, mixed oligonucleotide primers corresponding to the 5' leader (signal peptide) sequences and/or framework 1 (FR1) sequences, as well as primer to a conserved 3' constant region primer can be used for PCR amplification of the heavy and light chain variable regions from a number of murine antibodies (Larrick et al. (1991) *Biotechniques* 11:152-156). A similar

- 37 -

strategy can also been used to amplify human heavy and light chain variable regions from human antibodies (Larrick et al. (1991) *Methods: Companion to Methods in Enzymology* 2:106-110).

In an illustrative embodiment, RNA is isolated from activated B cells of, for
5 example, peripheral blood cells, bone marrow, or spleen preparations, using standard protocols (e.g., U.S. Patent No. 4,683,202; Orlandi, et al. *PNAS* (1989) 86:3833-3837; Sastry et al., *PNAS* (1989) 86:5728-5732; and Huse et al. (1989) *Science* 246:1275-1281.) First-strand cDNA is synthesized using primers specific for the constant region of the heavy chain(s) and each of the κ and λ light chains, as well as primers for the signal
10 sequence. Using variable region PCR primers, the variable regions of both heavy and light chains are amplified, each alone or in combination, and ligated into appropriate vectors for further manipulation in generating the display packages. Oligonucleotide primers useful in amplification protocols may be unique or degenerate or incorporate inosine at degenerate positions. Restriction endonuclease recognition sequences may also be incorporated into
15 the primers to allow for the cloning of the amplified fragment into a vector in a predetermined reading frame for expression.

The V-gene library cloned from the immunization-derived antibody repertoire can be expressed by a population of display packages, preferably derived from filamentous phage, to form an antibody display library. Ideally, the display package comprises a system
20 that allows the sampling of very large diverse antibody display libraries, rapid sorting after each affinity separation round, and easy isolation of the antibody gene from purified display packages. In addition to commercially available kits for generating phage display libraries (e.g., the Pharmacia *Recombinant Phage Antibody System*, catalog no. 27-9400-01; and the Stratagene *SurfZAP*TM phage display kit, catalog no. 240612), examples of methods and reagents particularly amenable for use in generating a diverse antibody display library can be found in, for example, Ladner et al. U.S. Patent No. 5,223,409; Kang et al. International
25 Publication No. WO 92/18619; Dower et al. International Publication No. WO 91/17271; Winter et al. International Publication WO 92/20791; Markland et al. International Publication No. WO 92/15679; Breitling et al. International Publication WO 93/01288; McCafferty et al. International Publication No. WO 92/01047; Garrard et al. International
30 Publication No. WO 92/09690; Ladner et al. International Publication No. WO 90/02809; Fuchs et al. (1991) *Bio/Technology* 9:1370-1372; Hay et al. (1992) *Hum Antibod Hybridomas* 3:81-85; Huse et al. (1989) *Science* 246:1275-1281; Griffiths et al. (1993) *EMBO J* 12:725-734; Hawkins et al. (1992) *J Mol Biol* 226:889-896; Clackson et al. (1991) *Nature* 352:624-628; Gram et al. (1992) *PNAS* 89:3576-3580; Garrad et al. (1991) *Bio/Technology* 9:1373-1377; Hoogenboom et al. (1991) *Nuc Acid Res* 19:4133-4137; and Barbas et al. (1991) *PNAS* 88:7978-7982.

- 38 -

In certain embodiments, the V region domains of heavy and light chains can be expressed on the same polypeptide, joined by a flexible linker to form a single-chain Fv fragment, and the scFV gene subsequently cloned into the desired expression vector or phage genome. As generally described in McCafferty et al., *Nature* (1990) 348:552-554, complete V_H and V_L domains of an antibody, joined by a flexible (Gly₄-Ser)₃ linker can be used to produce a single chain antibody which can render the display package separable based on antigen affinity. Isolated scFV antibodies immunoreactive with a peptide having activity of a CD100 antigen can subsequently be formulated into a pharmaceutical preparation for use in the subject method.

Once displayed on the surface of a display package (e.g., filamentous phage), the antibody library is screened with a CD100 antigen, or peptide fragment thereof, to identify and isolate packages that express an antibody having specificity for the CD100 antigen. Nucleic acid encoding the selected antibody can be recovered from the display package (e.g., from the phage genome) and subcloned into other expression vectors by standard recombinant DNA techniques.

The antibodies of the current invention can be used therapeutically to inhibit a B cell response through blocking receptor:ligand interactions necessary for transduction of a CD100 ligand-associated signal in the B cell. These so-called "blocking antibodies" can be identified by their ability to inhibit a B cell response when added to an *in vitro* assay as described herein. Antibodies of the invention can also be used to block a T cell response, such as T cell proliferation. Alternatively, the antibodies of the invention can be stimulatory antibodies, and stimulate a B cell and/or a T cell response.

The polyclonal or monoclonal antibodies of the current invention, such as an antibody specifically reactive with a recombinant or synthetic peptide having a CD100 activity can also be used to isolate the native CD100 antigen from cells. For example, antibodies reactive with the peptide can be used to isolate the naturally-occurring or native form of CD100 from activated B lymphocytes by immunoaffinity chromatography. In addition, the native form of cross-reactive CD100-like molecules can be isolated from B cells or other cells by immunoaffinity chromatography with an anti-CD100 antibody.

IV. Uses and Methods of the Invention

The invention further pertains to methods for modulating a leukocyte response in which a leukocyte is contacted *in vitro* or *in vivo* with an agent which modulates a CD100 ligand-associated signal. The term "leukocyte" is intended to include any cell of the blood which is not a red blood cell and includes lymphocytes, granulocytes, and monocytes. A preferred leukocyte is a lymphocyte, such as a B cell or a T cell.

The term "B cell" is intended to include a B lymphocyte that is at any state of maturation. Thus, the B cell can be a progenitor cell, a pre-B cell, an immature B cell, a mature B cell, a blast cell, a centroblast, a centrocyte, an activated B cell, a memory B cell,

- 39 -

or an antibody secreting plasma cell. A preferred B cell is an activated B cell, i.e., a B cell which has encountered an antigen. The term "B cell response" is intended to include a response of a B cell to a stimulus. The stimulus can be a soluble stimulus such as an antigen, a lymphokine, or a growth factor or a combination thereof. Alternatively, the stimulus can be membrane bound molecule, such as a receptor on T helper (Th) cells, e.g., CD28, CTLA4, gp39, or an adhesion molecule. Since a change in a B cell, such as a change occurring during the process of B cell maturation or activation is mediated by extracellular factors and membrane bound molecules, a response of a B cell is intended to include any change in a B cell, such as a change in stage of differentiation, secretion of factors, e.g., antibodies. Thus, a modulation of a B cell response can be a modulation of B cell aggregation, a modulation of B cell differentiation, such as differentiation into a plasma cell or into a memory B cell, or a modulation of cell viability. In a preferred embodiment, the invention provides a method for stimulating the differentiation of a B cell from a lymphoblast to a centrocyte. In another preferred embodiment, the invention provides a method for modulating B cell aggregation, such as homotypic B cell aggregation. In another embodiment, the invention provides a method for modulating B cell survival. In yet another preferred embodiment, the invention provides a method for modulating production of antibodies by B cells. In a further embodiment, the invention provides a method for modulating proliferation of B cells.

In one embodiment, the invention provides a method for stimulating a T cell response. A T cell response is intended to include stimulation of any change in the T cell that results from interaction with a soluble or membrane bound factor. Thus, a T cell response can be T cell proliferation, T cytotoxic activity, secretion of cytokines, differentiation or any T cell effector function.

In a preferred embodiment, the invention provides a method for stimulating T cell proliferation in the presence of a primary activation signal, comprising contacting a T cell with a CD100 antigen or active fragment thereof and a primary activation signal. The T cell can be a CD4+ T cell, a CD8+ T cell, a T helper cell (Th), or a cytotoxic T cell (Tc). Interaction between the T cell receptor (TCR)/CD3 complex and antigen presented in conjunction with either major histocompatibility complex (MHC) class I or class II molecules on an antigen-presenting cell initiates a series of biochemical events termed antigen-specific T cell activation. The term "T cell activation" is used herein to define a state in which a T cell response has been initiated or activated by a primary signal, such as through the TCR/CD3 complex, but not necessarily due to interaction with a protein antigen. A T cell is activated if it has received a primary signaling event which initiates an immune response by the T cell.

T cell activation can be accomplished by stimulating the T cell TCR/CD3 complex or via stimulation of the CD2 surface protein. An anti-CD3 monoclonal antibody can be used to activate a population of T cells via the TCR/CD3 complex. Although a number of

- 40 -

anti-human CD3 monoclonal antibodies are commercially available, OKT3 prepared from hybridoma cells obtained from the American Type Culture Collection or monoclonal antibody G19-4 is preferred. Similarly, binding of an anti-CD2 antibody will activate T cells. Stimulatory forms of anti-CD2 antibodies are known and available. Stimulation through CD2 with anti-CD2 antibodies is typically accomplished using a combination of at least two different anti-CD2 antibodies. Stimulatory combinations of anti-CD2 antibodies which have been described include the following: the T11.3 antibody in combination with the T11.1 or T11.2 antibody (Meuer, S.C. et al. (1984) *Cell* 36:897-906) and the 9.6 antibody (which recognizes the same epitope as T11.1) in combination with the 9-1 antibody (Yang, S. Y. et al. (1986) *J. Immunol.* 137:1097-1100). Other antibodies which bind to the same epitopes as any of the above described antibodies can also be used. Additional antibodies, or combinations of antibodies, can be prepared and identified by standard techniques.

A primary activation signal can also be provided by a polyclonal activator. Polyclonal activators include agents that bind to glycoproteins expressed on the plasma membrane of T cells and include lectins, such as phytohemagglutinin (PHA), concanavalin (Con A) and pokeweed mitogen (PWM).

A primary activation signal can also be delivered to a T cell through use of a combination of a protein kinase C (PKC) activator such as a phorbol ester (e.g., phorbol myristate acetate) and a calcium ionophore (e.g., ionomycin which raises cytoplasmic calcium concentrations). The use of these agents bypasses the TCR/CD3 complex but delivers a stimulatory signal to T cells. These agents are also known to exert a synergistic effect on T cells to promote T cell activation and can be used in the absence of antigen to deliver a primary activation signal to T cells.

Accordingly, the invention provides a method for stimulating antigen specific T cell proliferation by contacting a T cell with a stimulatory form of a CD100 antigen and a primary activation signal provided by an antigen presented in the context of a major histocompatibility complex antigen, such as on an antigen presenting cell. The invention further provides a method for stimulating proliferation of T cells in a non antigen specific manner by contacting the T cell with a CD100 antigen and an agent which provides a non antigen specific primary activation signal, such as an anti-CD3 antibody, a polyclonal activator, a combination of a PKC activator and a calcium ionophore, or an agent which stimulates CD2.

The invention provides methods for modulating a leukocyte response. The term "modulating" is intended to include stimulation or inhibition of a leukocyte response. In one embodiment, the invention provides a method for stimulating B cell aggregation. In another embodiment, the invention provides a method for inhibiting B cell aggregation. Also within the scope of the invention are methods for stimulating T cell proliferation and methods for inhibiting T cell proliferation.

- 41 -

In one embodiment of the invention, a leukocyte response is modulated by contacting leukocytes with an agent which modulates a CD100 ligand-associated signal. The term "CD100 ligand-associated signal" is intended to include an intracellular signal which is induced by contact of the natural form of CD100 with its ligand on an immune cell, such as a leukocyte and which results in the biological effects induced by such a contact, e.g., stimulation of B cell aggregation, stimulation of differentiation, increased cell viability, reduction of CD23 expression, and/or stimulation of T cell proliferation. The CD100 ligand-associated signal can be mediated by one receptor, or by several different receptors. The term "CD100 receptor" is used herein interchangeably with the term "CD100 ligand" and is intended to include a surface molecule or a secreted molecule with which a CD100 antigen interacts. Such an interaction can be a "positive interaction", i.e., resulting in transduction of a CD100 ligand-associated signal and the resulting biological effects. An interaction of a CD100 molecule with one of its receptors or ligands can also be a "negative interaction", such that upon interaction of the receptor with a CD100 molecule, no CD100 ligand-associated signal is transduced. Thus, a CD100 molecule may interact with more than one receptor, and the outcome of the interaction with the different receptors may be different according to the specific receptor. Specific types of leukocytes and other cells may have specific receptors. The outcome of the interaction of CD100 with one of its receptors may depend on the presence of other signals delivered to the leukocyte. One possible receptor for CD100 is CD100 itself, or a molecule having a CD100 activity and/or being structurally related to CD100.

A. Agents which stimulate a CD100 ligand-associated signal

In one embodiment of the invention, the agent which modulates a CD100 ligand-associated signal is an agent which stimulates a CD100 ligand-associated signal. A CD100 ligand-associated signal can be stimulated in a leukocyte by contact of the leukocyte with a stimulatory form of CD100. Alternatively, a CD100 ligand-associated signal can be stimulated by an agent which is not a form of CD100, but which mimicks the effects of a stimulatory form of CD100 and interacts with the CD100 ligand on the leukocyte. In yet another embodiment, a CD100 ligand-associated signal is stimulated by contacting a leukocyte with an agent which does not interact with CD100, but which mimicks a CD100 ligand-associated signal.

In a preferred embodiment of the invention, the stimulatory agent is a stimulatory form of a CD100 molecule. The term "stimulatory form of a CD100 molecule" is intended to include an agent which is a CD100 antigen, or molecule derived therefrom and which interacts with a leukocyte, such that a CD100 ligand-associated signal is transduced in the leukocyte.

A preferred CD100 stimulatory form of CD100 is a membrane bound form of CD100, or a form of CD100 linked to a solid phase surface. It has been shown (Examples

- 42 -

4 and 5 herein) that contacting a population of B cells with NIH-3T3 cells expressing CD100 results in augmentation of cell clustering and B cell survival. Thus, the invention provides methods for stimulating B cell aggregation, B cell differentiation, and increased B cell survival comprising contacting a population of B cells with cells that express CD100 molecules on their surface. It has further been shown herein that contacting a population of T cells with NIH-3T3 expressing CD100 in the presence of anti-CD3 antibodies results in stimulation of T cell proliferation. Accordingly, the invention also provides methods for stimulating T cell proliferation, comprising contacting a population of T cells with cells that express CD100 and a primary activation signal. Such cells can be cells which naturally express CD100 on their surface. Alternatively, the CD100 cells for practicing the invention can be cells that have been transfected to express a stimulatory form of CD100. In yet another embodiment, CD100 positive cells are obtained by linking a CD100 molecule to the cell surface, e.g., using cross-linking reagents. A stimulatory form of CD100 can also be linked to a solid phase support, such as a bead. The stimulatory form of a CD100 molecule can be the full length protein. Alternatively, the stimulatory form of CD100 is a stimulatory fragment of CD100. A stimulatory fragment of a CD100 molecule is a fragment of a CD100 molecule which upon interaction with B cells results in stimulation of a B cell response, such as B cell aggregation. Nucleic acids that can be used for preparing stimulatory forms of CD100 as well as methods for expressing these nucleic acids are described above. An assay for confirming that a form of CD100 is a stimulatory form of CD100 is also described above and in the Example section. Briefly, in one such assay, cells containing CD100 on their surface are added to a culture of B cells, and the effect on B cell aggregation is monitored either macroscopically or microscopically. A stimulatory form of a CD100 antigen can also be identified by performing a proliferation assay of T cells incubated in the presence of the form of CD100 to be tested and an anti-CD3 antibody. Alternatively, T cell proliferation can be measured by determining the amount of cytokines, such as IL-2 and IL-4 secreted by the T cells, such as by an ELISA assay. Methods for measuring T cell proliferation are known in the art and can be found for example in the published PCT applications Number PCT/US94/06255 and PCT/US94/08423.

Another preferred stimulatory form of CD100 is a soluble form of CD100. A soluble stimulatory form of CD100 can be prepared by recombinant techniques well known in the art. For example, for preparing a soluble stimulatory form of a CD100 molecule shown in Figure 2, a nucleic acid fragment having a sequence shown in Figure 1 (SEQ ID NO: 1) comprising the nucleic acid encoding the semaphorin domain and the Ig-like domain, i.e., about amino acid residues 22-630, 24-630, 22-731, 24-731, 42-630, or 42 to 731 of SEQ ID NO: 1, but not comprising the transmembrane and cytoplasmic domains is expressed in a host cell and purified according to methods known in the art. In a preferred embodiment, the soluble stimulatory form of a CD100 protein comprises a second peptide

- 43 -

which modifies the first peptide, such as to increase its stability. A preferred second peptide is an immunoglobulin fragment. These are further described herein.

Other agents which stimulate a CD100 ligand-associated signal in a cell include agents which mimmick the action of a stimulatory form of CD100 on a cell. Such agents
5 include small molecules which interact with a CD100 receptor or cell surface structure and deliver to the B cell a CD100 ligand-associated signal. Small molecules can be isolated from libraries of small molecules, such as combinatorial libraries, using *in vitro* assays, such as those described above for identifying fragments of CD100 which are capable of inducing a CD100-signal.

10 Methods within the scope of the invention pertain to the isolation of receptor(s) for CD100 molecules. Accordingly, additional agents which stimulate a CD100 ligand-associated signal in a B cell include agents which interact with the CD100 receptor and deliver a CD100 ligand-associated signal. Preferred stimulatory agents interacting with a CD100 receptor are antibodies to CD100 receptors which deliver to the B cell a CD100
15 ligand-associated signal. Such antibodies can be prepared as described herein for the preparation of anti-CD100 antibodies. Other agents which stimulate a CD100 ligand-associated signal include constitutively activated forms of CD100 receptors, that can be obtained, for example, by modifying the intracellular domain of the receptor, such that the modified receptor constitutively delivers a CD100 ligand-associated signal to the cell.

20 The interaction of a CD100 antigen with a leukocyte may result in stimulation of a leukocyte response through a signal delivered to the leukocyte from the CD100 receptor. Alternatively, the interaction of a leukocyte with a cell having a CD100 molecule on its surface may result in secretion of a soluble factor from the leukocyte or the cell having a CD100 molecule on its surface which then stimulates a leukocyte response. Thus, such a
25 soluble factor could also be used as an agent which stimulates a CD100 ligand-associated signal and is also within the scope of the invention. Methods for isolating such a soluble factor are also within the scope of the invention.

In the instance where CD100 is its own receptor, stimulatory agents could be agents which interact with CD100, such as antibodies to CD100, such as the antibodies BD16
30 (Herold C. et al, (1994), *Int. Immunol.* 7, 1.), BB18 (Bougeret C., et al., (1992), *J. Immunol.* 148, 318.), and F937G2 (Seed B., (1987), *Nature* 329, 840.). Antibodies which stimulate CD100 can be prepared according to methods described herein.

B. Agents which inhibit a CD100 ligand-associated signal

35 In another embodiment of the invention, the agent which modulates a CD100 signal in a leukocyte is an agent which inhibits a CD100 ligand-associated signal. Inhibitory agents include agents which block stimulatory agents from delivering a CD100 ligand-associated signal and agents which deliver a negative, or inhibitory signal to the cell. Such agents are termed herein "CD100 inhibitors".

- 44 -

Agents which block the transduction of a CD100 ligand-associated signal include agents which interact with a CD100 receptor but fail to deliver a CD100 ligand-associated signal, thereby preventing delivery of a CD100 ligand-associated signal by stimulatory agents. Preferred inhibitory agents include inhibitory forms of CD100 molecules. Such inhibitory forms can, e.g., bind a CD100 receptor, fail to deliver a positive signal and thereby inhibit a CD100 ligand-associated signal. Alternatively, the inhibitory form of CD100 could deliver a negative signal, further inhibiting a B cell response. Inhibitory forms of CD100 can be modified forms of CD100 molecules, fragments of CD100 molecules, or modified fragments. Inhibitory forms of CD100 antigens can be prepared by methods similar to those described herein for the preparation of stimulatory forms of CD100. An inhibitory form of CD100 will preferably comprise the extracellular domain of a CD100 molecule, or at least a portion of the extracellular domain that is necessary for interacting with the CD100 receptor. CD100 molecules or fragments thereof that retain binding capacity to CD100 receptors can then be mutated, such as by site directed mutagenesis for obtaining a form of CD100 or fragment thereof that retains binding capacity but fails to deliver a CD100 ligand-associated signal. The inhibitory efficiency of the inhibitory forms of CD100 can be determined, e.g., in an *in vitro* assay wherein B cells are incubated in the presence of a stimulatory form of CD100, such as NIH-3T3 cells expressing a full length CD100 molecule on the cell surface. Various amounts of the inhibitory form of CD100 to be tested are added to this assay and a B cell response, such as B cell aggregation is measured. An inhibitory form of CD100 will inhibit or at least reduce B cell aggregation. An inhibitory form of CD100 can also be identified as a form of CD100 which, when added to a culture of T cells in the presence of a primary T cell activation signal and a stimulatory form of CD100 inhibits T cell proliferation.

Additional agents within the scope of the invention which block the transduction of a CD100 ligand-associated signal include agents which interact with CD100 and thereby prevents its interaction with a CD100 receptor. Preferred inhibitory forms of CD100 include antibodies to CD100, such as blocking antibodies. Thus, blocking antibodies to CD100 will interact with CD100 and block its interaction with its ligand, thus inhibiting transduction of a signal from the CD100 ligand. Blocking antibodies can be prepared according to methods known in the art, using, for example, a soluble form of an extracellular domain of CD100 as the antigen. Also within the scope of the invention are soluble forms of CD100 receptors or fragments thereof or modified forms thereof which are capable of interacting with CD100 and blocking its interaction with a CD100 receptor on a cell. The soluble forms of CD100 receptors may also be linked to a solid phase surface. These soluble or membrane bound forms of CD100 receptors can be prepared and modified similarly to the soluble CD100 molecules described herein.

- 45 -

Additional inhibitory agents include small molecules. Thus, it is possible to isolate small molecules which inhibit a signal through CD100 from a library of small molecules using, for example, the assay described above. These molecules can block a CD100 ligand-associated signal by either interacting with CD100 or with its receptor, such that the interaction between CD100 and its receptor is inhibited. Alternatively, the small molecule may interact directly with the CD100 receptor and deliver a negative signal.

Preferred methods for inhibiting a CD100 ligand-associated signal in a leukocyte include contacting a leukocyte with a combination of at least two inhibitory agents. In a particularly preferred embodiment, the method includes contacting a leukocyte with at least one inhibitory agent which interacts with CD100 and with at least one inhibitory agent which interacts with a CD100 receptor.

Other inhibitory agents include CD100 antisense molecules and ribozymes. Thus, delivery of a CD100 ligand-associated signal by a cell expressing CD100 can be inhibited in a cell, such as a B cell or a T cell, by introducing and/or expressing CD100 antisense molecules or ribozymes. Antisense molecules and ribozymes are further described herein. Alternatively, a CD100 ligand-associated signal can be blocked in a cell, such as a B cell or a T cell by blocking the expression of a ligand for CD100 in the cell. Blocking or at least reducing the expression of a CD100 ligand can be obtained by introducing and/or expressing in the T or B cell antisense molecules interacting with a CD100 ligand.

C. Modulation of a B cell response by modulation of a CD100 ligand-associated signal and a CD40 signal

The invention further provides methods for modulating a B cell response comprising contacting the population of cells with a first agent which modulates a CD100 ligand-associated signal and a second agent which modulates a CD40 signal. Similarly to CD100 stimulation, resting B cells receiving a CD40 mediated contact dependent signal from CD40L on activated T cells are stimulated to aggregate, cluster, and proliferate (Banchereau J. et al., (1994), *Annu. Rev. Immunol.* 12, 881; Clark E. A. et al, (1994), *Nature* 367, 425. As also shown herein (Example 4), CD40 ligand (CD40L) transfectants (t-CD40L) induce B cells to aggregate and form clusters. It has been shown herein that B cell aggregation and cell survival induced by stimulation of B cells through CD100 is synergistically increased by simultaneously stimulating the cells through CD40. Thus, in a preferred method of the invention, a population of cells is contacted with an agent which provides a stimulatory signal through CD100 and an agent which provides a stimulatory signal through CD40. Also within the scope of the invention are methods for inhibiting a B cell response comprising contacting B cells with at least one first agent which inhibits a CD100 signal and at least one second agent which inhibits a CD40 signal, such that a B cell response is inhibited.

- 46 -

D. Additional methods of use of CD100 antigens

In another embodiment of the invention, the B cells which are contacted with an agent which stimulates a CD100 ligand-associated signal are further contacted with T cells. Thus, since CD100 provides a costimulatory signal to T cells, these T cells will provide
5 help to the B cells for further stimulating a B cell response. In yet another embodiment, the population of cells comprising B and T cells further comprises at least one primary activation signal, such as an antigen, for example on an antigen presenting cell, or an anti-CD3 antibody.

The methods of the invention can be practiced *in vitro* or *in vivo*. For example a
10 stimulatory form of a CD100-like molecule can be added to a culture of B cells, such as a hybridoma culture, such that the production of antibodies by the hybridomas is increased. Alternatively, the molecules of the invention can be added to a population of T cells, such that their proliferation *in vitro* is stimulated. The molecules of the invention can also be added to a culture of primary B cells or T cells obtained from an individual for stimulating
15 their differentiation and proliferation, respectively.

V. Applications of the Invention

The invention provides a method for modulating a leukocyte response comprising contacting the leukocytes with an agent which modulates a CD100 ligand-associated signal
20 in the leukocytes. In one embodiment, the invention provides a method for stimulating a B cell response. Stimulation of a B cell response can result in increased B cell aggregation, increased B cell differentiation and/or increased B cell survival. The B cells can, for example, be stimulated to differentiate from a lymphoblast to a centroblast or centrocyte and thereby stimulate the differentiation of B cells into either antibody secreting plasma
25 cells or memory B cells. In another embodiment, the invention provides a method for stimulating a T cell response, such as T cell proliferation. In a preferred embodiment, the invention provides a method for stimulating a B cell response and a T cell response, such as T cell proliferation. Thus, the presence of a stimulatory form of CD100 in a population of cells comprising both B cells and T cells should further amplify the B cell response
30 stimulated by CD100. It will be appreciated that it is particularly advantageous to stimulate both B cells and T cells for most applications.

In one embodiment, the invention provides a method of vaccination. Accordingly, a subject in need of vaccination is given a dose of at least one antigen in the presence of a therapeutically effective amount of an agent which stimulates a CD100 ligand-associated
35 signal. The antigen and the stimulatory agent are preferably administered simultaneously. Alternatively, the antigen and the stimulatory agent are administered separately, such that, for example, the antigen is administered prior to the stimulatory agent. In a preferred embodiment, the subject is subsequently boosted at least once with additional doses of antigen and the stimulatory agent. The antigen can be any molecule, or structure against

- 47 -

which it is desirable to have a strong and rapid immune reaction. Thus, antigens within the scope on the invention include viral antigens, bacterial antigens, tumor antigens, or any antigens, or combination of antigens from any organism. An agent which stimulates a CD100 ligand-associated signal can be added to any classic vaccine composition for preventing an infection in a subject.

In a preferred embodiment, the vaccine formulation further comprises a therapeutically effective dose of an agent which stimulates CD40. Thus, the subject is contacted with at least one antigen, an agent which stimulates a CD100 ligand-associated signal and an agent which stimulates CD40. In a preferred embodiment, the CD40 and the agent which stimulates a CD100 ligand-associated signal are administered together to the subject, which is also preferably administered together with the antigen(s). Further boosting of the subject with the antigen(s) is preferably performed by administering the antigen(s) and the stimulatory CD40 agent and/or the agent which stimulates a CD100 ligand-associated signal.

An agent which stimulates a CD100 ligand-associated signal can also be used for treating disorders in which boosting of a B cell response is beneficial. Such disorders include infections by pathogenic microorganisms, such as bacteria, viruses, and protozoans. Preferred disorders for treating according to the method of the invention include extracellular bacterial infections, wherein bacteria are eliminated through opsonization and phagocytosis or through activation of the complement. Other preferred infections that can be treated according to the method of the invention include viral infections, including infections with an Epstein-Barr virus or retroviruses, e.g., a human immunodeficiency virus.

In another embodiment of the invention, an agent which stimulates a CD100 ligand-associated signal can be administered to a subject having an antibody deficiency disorder resulting, for example, in recurrent infections and hypogammaglobulinemia (Ochs et al. (1989) Disorders in Infants and Children, Stiehm (ed.) Philadelphia, W.B. Sanders, pp 226-256). These disorders include common variable immunodeficiency (CVI), hyper-IgM syndrome (HIM), and X-linked agammaglobulinemia (XLA). Some of these disorders, e.g., HIS, are caused by a mutation in the CD40 ligand, gp39, on the T cell and administration of an agent which stimulates a CD100 ligand-associated signal would thus compensate for at least some of the B cell deficiencies, such as stimulation of B cell differentiation.

Furthermore, upregulation of a B cell response is also useful for treating a subject with a tumor. In one embodiment, an agent which stimulates a CD100 ligand-associated signal is administered at the site of the tumor. In another embodiment, an agent which stimulates a CD100 ligand-associated signal is administered systemically.

In another embodiment, the invention provides a method for stimulating B cells in culture, such as hybridoma cells. In a preferred embodiment, stimulation of the population

- 48 -

of B cells results in increased antibody production. Thus, an agent which stimulates a CD100 ligand-associated signal can be added at an effective dose to a B cell culture, such as a hybridoma, such that antibody production by the B cells is enhanced. The effective dose of the agent which stimulates a CD100 ligand-associated signal to be added to the culture can easily be determined experimentally. This can be done, for example, by adding various amounts of the agent to a constant amount of B cells, and by monitoring the amount of antibody produced, e.g., by ELISA. The effective dose corresponds to the dose at which highest amounts of antibodies are produced.

In yet another embodiment, an agent which stimulates a CD100 ligand-associated signal is administered together with a hybridoma into the peritoneal cavity of a mouse, such that the amount of antibody produced by the hybridoma is increased.

In another embodiment of the invention, a T cell is contacted with an agent which stimulates a CD100 ligand-associated signal and a primary activation signal, such that T cell proliferation is increased. The primary activation signal can be an antigen, or a combination of antigens, such that proliferation of one or more clonal populations of T cells is stimulated. Alternatively the primary activation signal can be a polyclonal agent, such as an antibody to CD3, such that T cell proliferation is stimulated in a non clonal manner.

In one embodiment, the invention provides a method for expanding a population of T cells *ex vivo*. Accordingly, primary T cells obtained from a subject are incubated with an agent which stimulates CD100 ligand-associated signal and a primary activation signal. Following activation and stimulation of the T cells, the progress of proliferation of the T cells in response to continuing exposure to the agent which stimulates a CD100-induced signal is monitored. When the rate of T cell proliferation decreases, the T cells are reactivated and restimulated, such as with additional anti-CD3 antibody and an agent which stimulates a CD100-induced signal in the T cell, to induce further proliferation. The monitoring and restimulation of the T cells can be repeated for sustained proliferation to produce a population of T cells increased in number from about 100- to about 100,000-fold over the original T cell population. Methods for stimulating the expansion of a population of T cells are further described in the published PCT application PCT/US94/06255 and can be practiced by using an agent which is capable of stimulating a CD100 ligand-associated signal as the costimulatory molecule. In a preferred embodiment, T cell expansion is obtained by incubating the T cells with a primary activation signal and at least two costimulatory signals, such as a molecule providing a costimulatory signal through a CD28 or CTLA4 receptor, such as B7-1 or B7-2, and a costimulatory molecule that stimulates a CD100 ligand-associated signal.

The method of the invention can be used to expand selected T cell populations for use in treating an infectious disease or cancer. The resulting T cell population can be genetically transduced and used for immunotherapy or can be used for *in vitro* analysis of infectious agents such as HIV. Proliferation of a population of CD4⁺ cells obtained from

- 49 -

an individual infected with HIV can be achieved and the cells rendered resistant to HIV infection. Following expansion of the T cell population to sufficient numbers, the expanded T cells are restored to the individual. The expanded population of T cells can further be genetically transduced before restoration to a subject. Similarly, a population of tumor-infiltrating lymphocytes can be obtained from an individual afflicted with cancer and the T cells stimulated to proliferate to sufficient numbers and restored to the individual. In addition, supernatants from cultures of T cells expanded in accordance with the method of the invention are a rich source of cytokines and can be used to sustain T cells *in vivo* or *ex vivo*.

In another embodiment of the invention, T cell proliferation is stimulated *in vivo*. In a preferred embodiment, an agent which stimulates a CD100 ligand-associated signal in the T cell is administered to a subject, such that T cell proliferation in the subject is stimulated. The subject can be a subject that is immunodepressed, a subject having a tumor, or a subject infected with a pathogen. The agent of the invention can be administered locally or systemically. The agent can be administered in a soluble form or a membrane bound form. Additional applications for an agent capable of providing a costimulatory signal to T cells, such that their proliferation is stimulated, are described in the published PCT applications PCT/US94/13782 and PCT/US94/08423, the content of which are incorporated herein by reference.

The invention further provides inhibitors of a CD100 ligand-associated signal. In a specific embodiment, an inhibitory CD100 agent is used for prolonging graft survival. Thus, a therapeutically effective dose of an inhibitor of a CD100-signal is administered to a recipient of an allotypic or xenotypic graft, such that graft survival is prolonged at least in part by reducing a B cell response to the graft. In a preferred embodiment, the inhibitor of a CD100 ligand-associated signal is administered prior to transplantation of the graft, such that B cell responses are downregulated at the time of transplantation. Alternatively, the inhibitor of a CD100-signal can be administered at about the same time as transplantation of the graft or after transplantation of the graft. In preferred embodiments, the inhibitor of a CD100-signal is administered together with an inhibitor of a CD40-induced signal to further block B cell responses. Additional agents, such as agents which block T cell activation and clonal expansion, can also be administered to the graft recipient. Such agents include antibodies to B7-1, B7-2, a combination thereof, and CTLA4Ig.

In yet another embodiment of the invention, an inhibitor of a CD100 signal can be used to prevent graft versus host disease (GVHD). In a preferred embodiment, the donor bone marrow is incubated with an inhibitor of a CD100-signal prior to administration to the recipient. The treatment can further include administration of a therapeutically effective dose of a CD100 inhibitor to the bone marrow recipient prior to and/or after bone marrow transplantation. As described in the treatment for prolonging graft survival, the CD100 inhibitor can be used together with a CD40 inhibitor and/or with yet additional agents.

- 50 -

Inhibitors of CD100 can also be used to reduce B cell and/or T cell responses in autoimmune diseases which involve autoreactive B and/or T cells. Accordingly, administration of an inhibitor of CD100 to a subject can be used for treating a variety of autoimmune diseases and disorders having an autoimmune component, including diabetes mellitus, arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis), multiple sclerosis, myasthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), psoriasis, Sjögren's Syndrome, including keratoconjunctivitis sicca secondary to Sjögren's Syndrome, alopecia areata, allergic responses due to arthropod bite reactions, Crohn's disease, aphthous ulcer, iritis, conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma, allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis, proctitis, drug eruptions, leprosy reversal reactions, erythema nodosum leprosum, autoimmune uveitis, allergic encephalomyelitis, acute necrotizing hemorrhagic encephalopathy, idiopathic bilateral progressive sensorineural hearing loss, aplastic anemia, pure red cell anemia, idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis, chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue, lichen planus, Crohn's disease, Graves ophthalmopathy, sarcoidosis, primary biliary cirrhosis, uveitis posterior, and interstitial lung fibrosis.

The efficacy of a CD100 inhibitor in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

It is possible to treat a subject having an allergy with an agent, such as an agent which blocks a CD100 ligand-associated signal, which inhibits or reduces production of IgE antibodies to thereby ameliorate the allergic reaction. Allergic reactions may be systemic or local in nature, depending on the route of entry of the allergen and the pattern of deposition of IgE on mast cells or basophils. Thus, in various embodiments for treating allergies, the agent is administered either systemically or locally. Alternatively, the allergen can be administered together with an agent which blocks a CD40 signal. The treatment can further comprise administration of an agent which neutralizes IL-4, such as an anti-IL4 antibody.

Additional disorders for which the agents of the invention provide a treatment include lymphomas which are characterized by abnormal B cells. It has been shown by immunohistopathology that some lymphomas are characterized by high expression of CD100, whereas other types of lymphomas are characterized by low level expression of CD100. Lymphomas characterized by a block in B cell differentiation express low levels

- 51 -

of CD100. Thus, agents which stimulate a CD100 ligand-associated signal can be used to treat lymphomas which are characterized by a block in B cell differentiation, such that differentiation of the lymphoma cells is stimulated. Such lymphomas are characterized by small, well-differentiated lymphocytes and include low-grade lymphomas, such as small lymphocytic and follicular lymphomas. In one embodiment of the invention, an agent which stimulates a CD100 ligand-associated signal, such as a soluble stimulatory form of CD100, is administered to a subject having a low grade lymphoma, such that differentiation of the lymphoma cells is stimulated. Lymphomas characterized by an excessive proliferation and/or differentiation of B cell differentiation express high levels of CD100. Thus, inhibitors of CD100 can be used for treating a subject having a lymphoma characterized by an excessive proliferation and/or differentiation of B cells, such that their proliferation and/or differentiation is inhibited. Such lymphomas are characterized by larger, poorly differentiated lymphocytes and large lymphocytes with characteristics of a histiocyte or lymphoblast and include : intermediate grade lymphomas, such as follicular large cell, diffuse small cleaved cell, diffused mixed cell, and diffuse large cell lymphomas; high grade lymphomas, such as immunoblastic, small noncleaved (Burkitt's and non-Burkitt's), lymphoblastic, and true histiocytic lymphomas. In one embodiment, an inhibitor of CD100 is administered to a subject having a large cell lymphoma, such that proliferation and/or differentiation of the lymphoma cells is inhibited.

Additional applications for an agent capable of inhibiting a costimulatory signal in T cells, such that T cell proliferation is inhibited, are described in the published PCT applications PCT/US94/13782 and PCT/US94/08423, the content of which are incorporated herein by reference.

In preferred embodiments of the invention agents which modulate a CD100 ligand-associated signal are preferably administered to subject together with agents which modulate other costimulatory signals. For example, in a method for preventing graft rejection, it is preferable to administer to a subject having been transplanted an agent which inhibits a CD100 ligand-associated signal together with agents which inhibit a costimulatory signal delivered by a member of the B7 family of proteins, such as B7-1 and B7-2. In a preferred embodiment, an agent which blocks a CD100 associated signal is administered together with anti-B7-1 and/or anti-B7-2 antibodies, or CTLA4Ig. The method can further comprise administering to the subject additional agents, such as agents which inhibits the interaction of growth or differentiation factors with their receptors.

Also within the scope of the invention are diagnostic methods. It has been shown, for example, that B cell lymphomas are associated with a high level of CD100 expression. Thus, determining the level of CD100 expression in a lymph node section from a patient having enlarged lymph nodes using an agent that binds CD100 could be indicative of lymphoma. Detection of CD100 can also be performed using a nucleic acid probe that selectively recognizes the gene encoding CD100. A specific probe can be a portion of a

- 52 -

nucleic acid having a SEQ ID NO: 1. Other disorders associated with a high level of CD100, a CD100 ligand, a CD100-like molecule or receptor thereof could similarly be detected using agents of the invention.

Since the semaphorin domain of CD100 shares some homology with other semaphorin family members, such as H-Sema III and M-Sema C, it is likely that CD100 interacts with at least some of these neurological semaphorins. However, since the semaphorins identified in the nervous system act as chemorepellants, it is possible that CD100 is repulsive towards these neurological semaphorins. Thus, whether CD100 or CD100 ligand(s) act as chemorepellants or chemoattractants vis a vis the neurological semaphorins, blocking the interaction between an immune semaphorin, or receptor thereof, and a neurologic semaphorin, or receptor thereof, will result in modulation of the interaction between the immune and the nervous system. Such a modulation will be of interest in treating diseases characterized by an abnormal interaction between the immune and nervous systems.

Furthermore, if CD100 or its receptor(s) is capable of interacting with or repulsing neurologic semaphorins, the agents of the invention can be used for treating neurological diseases. Thus, depending on the disease to be treated, an agent of the invention which blocks or which stimulates interaction between neurons can be administered to a subject having the disease. Applications for CD100 agents or ligands in neurology include treatments for nerve damages, such as spinal cord injuries. The agents of the invention can also be used to direct regenerating neurons to their target.

Semaphorins are expressed during embryonic development. Thus, since CD100 is structurally related to at least some semaphorins, CD100 may also be involved in embryogenesis. Thus, CD100 agents could be useful in the regeneration of tissues or organs.

The invention can also be used to isolate one or more ligands of CD100 or CD100-like molecules. Various methods can be used for isolating ligands of CD100. A preferred method for isolating a CD100 ligand comprises screening of an expression library with CD100, such as a soluble form of CD100, according to methods known in the art. The expression library can be prepared from various tissues, preferably leukocytes, and even more preferably B lymphocytes. Thus, according to this method, a cDNA expression library is constructed using mRNA from B lymphocytes and the library is transfected into cells, preferably COS cells. The transfected cells are then incubated with a soluble form of CD100 that is tagged, e.g., with a biotin molecule. Cells binding CD100 are then detected by incubating the cells with a secondary reagent that is labelled and the cells are sorted by FACS analysis or using magnetic beads coated with a reagent that reacts with the CD100 labelled cells. The plasmids containing the cDNA are extracted, retransfected into COS cells, and rescreened with CD100. Following several rounds of screening, the plasmids are isolated and the insert is sequenced. A basic expression cloning technique has been

- 53 -

described by Seed and Aruffo, *Proc. Natl. Acad. Sci. USA*, 84:3365-3369 (1987) and Aruffo and Seed, *Proc. Natl. Acad. Sci. USA*, 84:8573-8577 (1987), although modifications to this technique may be necessary. The technique is also described in the published PCT application PCT/US94/08423.

VI. Pharmaceutical Compositions

The CD100 proteins and other agents described herein can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the protein or agent and a pharmaceutically acceptable carrier. As used herein the term "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

In one embodiment, the agents of the invention can be administered to a subject to modulate a B cell response in the subject, e.g., for stimulating the clearance of a pathogen from the subject. The agents are administered to the subjects in a biologically compatible form suitable for pharmaceutical administration *in vivo*. By "biologically compatible form suitable for administration *in vivo*" is meant a form of the agents, e.g., protein to be administered in which any toxic effects are outweighed by the therapeutic effects of the agent. The term "subject" is intended to include living organisms in which an immune response can be elicited, e.g., mammals. Examples of subjects include humans, dogs, cats, mice, rats, and transgenic species thereof. Administration of a therapeutically active amount of an agent of the present invention is defined as an amount effective, at dosages and for periods of time necessary to achieve the desired result. For example, a therapeutically active amount of a stimulatory form of a CD100 molecule, alone or together with a stimulatory form of a CD40 ligand, may vary according to factors such as the disease state, age, sex, and weight of the subject, and the ability of agent to elicit a desired response in the subject. Dosage regimens may be adjusted to provide the optimum therapeutic response. For example, several divided doses may be administered daily or the dose may be proportionally reduced as indicated by the exigencies of the therapeutic situation.

The agent may be administered in a convenient manner such as by injection (subcutaneous, intravenous, etc.), oral administration, inhalation, transdermal application, or rectal administration. Depending on the route of administration, the agent may be coated in a material to protect it from the action of enzymes, acids and other natural conditions which may inactivate the agent. For example, solutions or suspensions used for parenteral,

- 54 -

intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

To administer an agent by other than parenteral administration, it may be necessary to coat the agent with, or co-administer the agent with, a material to prevent its inactivation. For example, a stimulatory form of a CD100-like molecule may be administered to a subject in an appropriate carrier or diluent co-administered with enzyme inhibitors or in an appropriate carrier such as liposomes. Pharmaceutically acceptable diluents include saline and aqueous buffer solutions. Enzyme inhibitors include pancreatic trypsin inhibitor, diisopropylfluorophosphate (DEP) and trasylol. Liposomes include water-in-oil-in-water emulsions as well as conventional liposomes (Strejan *et al.*, (1984) *J. Neuroimmunol* 7:27). Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations may contain a preservative to prevent the growth of microorganisms.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In all cases, the composition must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

- 55 -

Sterile injectable solutions can be prepared by incorporating the agent in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the agent into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient (e.g., peptide) plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These may be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and

- 56 -

directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

5 This invention is further illustrated by the following Exemplification which should not be construed as limiting. The contents of all references and published patent applications cited throughout this application are hereby incorporated by reference.

EXEMPLIFICATION

Example 1: Isolation of a cDNA encoding CD100

10 A cDNA encoding a human CD100 antigen was isolated by COS cell expression cloning using an anti-CD100 antibody. A cDNA library was constructed in pCDM8 (Aruffo A et al, (1987), *Proc. Natl. Acad. Sci. USA* 84, 8573; Seed B et al, (1987), *Proc.*
15 *Natl. Acad. Sci. USA* 84, 3365) using poly (A)+RNA from PHA activated human T cells and size selected for inserts greater than 3 kb. The library was introduced into COS cells by DEAE-dextran transfection and CD100 expressing cells selected by two rounds of immunoselection and panning with CD100 mAb BD16 (Herold C. et al, (1994), *Int.*
Immunol. 7, 1). Twelve of 16 plasmids isolated contained a 4.2kB Xba insert and COS
20 cells individually transfected bound to BD16 but not to control Mouse IgG₁.

To confirm that the isolated 4.2 kb cDNA encodes CD100, COS cells were transiently transfected with the 4.2 kb CD100 cDNA, pCDM8 vector alone, and B7-1 cDNA. After 48 hours, cells were stained with antibodies against CD100 - BD16 (Herold C. et al, (1994), *Int. Immunol.* 7, 1), BB18 (Bougeret C et al., (1992), *J. Immunol.* 148, 318)
25 and F937G2 (Seed B., (1987), *Nature* 329, 840), and an isotype matched B7-1 antibody, B1.1. Binding of the mAbs was detected by indirect immunofluorescence using goat anti-mouse IgG₁-phycoerythrin and analyzed by flow cytometry. Figure 5, which represents the results of the flow cytometry analysis, show that the COS cells transfected with the 4.2 kb cDNA bind specifically to three monoclonal antibodies (mAbs) directed against CD100
30 (Herold C et al, in *Leucocyte Typing V*, S. F. Schlossman, et al., Eds. (Oxford University Press, Oxford, 1995), vol. 1, pp. 50), but not to control mAbs. Non transfected COS cells do not stain with the anti-CD100 antibodies. These results indicate that the 4.2 kb cDNA encodes CD100.

35 Further confirmation that the isolated 4.2kb cDNA encodes CD100 was provided by immunoprecipitation experiments. CHO cells were stably transfected with CD100 cDNA or vector alone and ¹²⁵I labeled. Cell lysates were immunoprecipitated with BB18 antibody or a control antibody, IgG₁, and separated on an 8.5% SDS-PAGE gel. The results indicate that a 150 kDa protein is immunoprecipitated from CHO cells transfected with CD100 and from activated T cells, but not from untransfected CHO cells. Activated B

- 57 -

cells also express a 150 kDa protein that is immunoprecipitated with an anti-CD100 antibody.

The nucleotide sequence of CD100 was determined for both strands of the original 4.2 kb clone and another clone 4.2H which was isolated from the same library by hybridization. The sequencing was carried out using synthetic oligonucleotide primers and dye-labeled terminator/Taq polymerase chemistry, and analyzed on an automated fluorescent DNA sequencer (Applied Biosystems). The sequence of the CD100 cDNA reveals a single long open reading frame of 2.6 kb, which is represented in Figure 1. Initiation of translation is likely to occur at the second ATG which, unlike the first ATG, is in a favorable context for translation initiation (Kozak M., (1995), *Proc. Natl. Acad. Sci. USA* 92, 2662; Kozak M., (1989), *J. Cell. Biol.* 108, 229). The CD100 sequence is deposited in Genbank under accession number

A BLAST (Altschul S. F. et al, (1990), *J. Mol. Biol.* 215, 403) search of the protein database indicated that CD100 is a novel protein, which has some homology to the semaphorin gene family. The amino acid sequence deduced from the 4.2 kb CD100 cDNA was compared to sequences using CLUSTAL. Figure 2 represents a comparison of the H-Sema III and mouse Sema C (M-Sema C) amino acid sequences. CD100 shares 39% identity with H-sema III in the sema domain and 33% identity in the Ig-like domain, whereas the rest of the protein is strikingly divergent. As seen in Figure 3, the CD100 protein consists of a signal sequence followed by a sema domain, an Ig domain, a lysine-rich stretch of 104 amino acids, a hydrophobic transmembrane region and a cytoplasmic tail of 110 amino acids. A consensus site for tyrosine phosphorylation, KPALTGY at amino acid 813 in the cytoplasmic tail supports the predicted association of CD100 with a tyrosine kinase (Sidorenko S et al, "Identification of antigens associated with protein kinases by activation antigens panel mAb." S. F. Schlossman, et al., Eds., *Leucocyte Typing V* (Oxford University Press, Oxford, 1995), vol. 1; Rudd C et al., "Identification of antigens associated with protein kinases by activation antigen panel mAb." S. F. Schlossman, et al., Eds., *Leucocyte Typing V* (Oxford University Press, Oxford, 1995), vol. 1). CD100 contains 15 of the 16 conserved sema domain cysteines and 9 putative N-linked glycosylation sites.

Thus, CD100 is a novel leukocyte semaphorin-like protein.

Example 2: CD100 is expressed on activated B and T cells and in non hematopoietic tissues

The level of CD100 mRNA was measured in several tissues by Northern blot analysis. 5 µg poly(A)+ RNA from activated B cells, Raji cells and activated T cells was separated by electrophoresis, transferred onto blots and hybridized with labeled 4.2 kb CD100 cDNA. These results indicate that CD100 expression is high in activated B and T cells and in Raji cells. Expression of CD100 is low in resting B and T cells. Furthermore,

- 58 -

this experiment showed the presence of two RNA species: one predominant species of about 4.5kb and a second species of about 9 kb.

Expression of CD100 was also analysed in various non hematopoietic tissues by Northern blot analysis. For this example, 2 µg of poly(A)+ RNA was separated, blotted and hybridized with labeled 4.2kb CD100 cDNA. The results indicate that CD100 mRNA is expressed in many non-hematopoietic tissues including the heart, brain, placenta, lung, skeletal muscle, kidney and pancreas, but not the liver. Interestingly, the four major transcripts of 3.8, 4.5, 7 kb, and 10 kb are differentially expressed with a distinct tissue distribution of transcripts. In most of these tissues, the major transcript was the 4.5kb species. Heart and muscle express essentially the 3.8kb transcript. This transcript was also found to be expressed in brain, together with the other major transcripts.

Example 3: CD100 is primarily expressed in activated B cells within the lymphoid follicle germinal center

In this example, the level of CD100 protein was measured in lymphoid tissues by immunohistochemistry.

Cryostat sections of lymphoid tissue were fixed in acetone for ten minutes, washed with PBS and incubated for one hour with the following primary antibodies: a mouse monoclonal antibody against CD100, a mouse monoclonal antibody against CD20, a pan-B cell marker, and a monoclonal antibody against CD3, a pan-T cell marker. The sections were then washed with PBS, incubated with biotinylated horse anti-mouse antibody (Vector Laboratories, Burlingame, CA) for 30 minutes, washed with PBS, incubated with avidin:biotinylated-peroxidase complex (Vector Laboratories, Burlingame, CA) for 40 minutes, and reacted with diaminobenzidine/hydrogen peroxide. Sections were subsequently stained with 2% methyl green.

The results show that anti-CD100 mAb staining is primarily in the germinal center (GC), sporadic in the interfollicular areas and virtually absent in the mantle zone (MZ). This pattern differs from antibodies which stain with a dendritic cell pattern (e.g. CD23) and is consistent with B cell surface staining. On the contrary, a mAb against the B cell restricted molecule, CD20, stains most cells in both the GC and the MZ and a mAb against the T cell restricted molecule, CD3, stains cells in the interfollicular areas but very few cells in the GC and MZ. For comparison, a lymphoid tissue section was fixed in 10% buffered formaldehyde, paraffin embedded, sectioned and stained with hematoxylin and eosin. This section shows a germinal center and mantle zone of a secondary lymphoid follicle with interfollicular T cell zone. Thus, the results of this experiment indicate that the major hematopoietic cell type that encounters CD100 in the GC is the B lymphocyte. Furthermore, given the paucity of T cells in this lymphoid compartment, the major source of CD100 in the GC is likely to be activated B cells.

- 59 -

Thus, consistent with the high levels of CD100 mRNA expression in activated B cells, anti-CD100 mAb predominantly stained activated B cells within the lymphoid follicle germinal center.

5 **Example 4: CD100 stimulates B cell homotypic aggregation and synergizes with CD40L**

The effect of CD100 on B cells, was analyzed in an *in vitro* model system using stable CD100 transfectants (t-CD100). NIH-3T3 cells were mock transfected, transfected with CD100 cDNA or with CD40L cDNA. Transfected cells were harvested, irradiated
10 (96Gy), plated at a fixed concentration of 10^5 total transfectants/well and incubated overnight. Human splenic B cells were cultured on the different transfectants at 10^6 B cells per 1 ml culture in 24-well plates in B cell medium (Carriere D et al., (1989), *Exp. Cell. Res.* 182, 114). Photographs of cell cultures were taken at a magnification of 100X at 72 hrs.

15 As shown in Figure 6d, the results of this example indicate that co-culture of human tonsillar B cells with irradiated t-CD100 stimulates the B cells to homotypically aggregate within 24 hours and form continually increasing clusters that are maximal in size by day 3. In contrast, no significant clusters were observed in the mock transfected controls (Figure 6a). Other B cell sources including splenic B cells, follicular lymphoma, and acute
20 lymphoblastic leukemias are similarly induced to cluster by co-culture with t-CD100. Figure 6b, indicates that CD40L transfectants (t-CD40L) also induce B cells to aggregate and form clusters. To examine the outcome of combining CD40L and CD100 signals, B cells were cultured on equal numbers of t-CD100 and t-CD40L, i.e., 50% t-CD100/50% t-CD40L (hereinafter referred to as t-CD100/t-CD40L). The total number of transfectants
25 was constant (i.e., identical to number plated in the t-mock, t-CD40L, or t-CD100 wells). Figure 6f shows that the combination of CD100 and CD40L signaling synergizes to give rise to extraordinarily large B cell clusters that were larger than those observed with either transfectant alone or with the control. Other ratios of transfectants were also examined (75% t-CD100/25% t-CD40L and 25% t-CD100/75% t-CD40L) and these consistently
30 induce larger clusters than observed with t-CD40L or t-CD100 alone, or the equivalent t-mock/t-CD40L control. Taken together, these results demonstrate that CD100 can directly induce B cell cluster formation, moreover, and that, when the CD100 and CD40L signals are combined, cluster formation is markedly enhanced.

The adhesion molecules LFA-3, LFA-1 and ICAM-1 are not upregulated by t-
35 CD100 or t-mock whereas t-CD40L upregulates these adhesion molecules on human B cells (Carriere D et al., (1989), *Exp. Cell. Res.* 182, 114). Furthermore, these adhesion molecules were similarly upregulated on tonsillar B cells following culture on t-mock/t-CD40L or t-CD100/t-CD40L. Thus, these results indicate that the CD100 induced B cell aggregation is not mediated by an increase in LFA-3, LFA-1, or ICAM-1. However, these

- 60 -

results do not exclude the possibility that other adhesion molecules might be responsible for this observation or alternatively that cluster formation results from the induction of conformational changes in adhesion molecules (Chan B.M. et al, (1991), *J. Immunol.* 147, 398).

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Example 5: CD100 alone or with CD40L stimulates an increase in B cell survival

To determine whether t-CD100/t-CD40L had an effect on B cell survival and/or proliferation, the number of viable B cells was determined by Trypan blue exclusion analysis after 3 days of co-culture according to the conditions described above. As shown
10 in Fig. 7, co-culture with t-mock cells resulted in significant numbers of B cells dying during the culture period. Co-culture with t-CD100 increased the number of viable cells compared to t-mock, but there were consistently fewer cells than observed with t-CD40L. t-CD100/t-CD40L stimulation consistently resulted in significantly greater numbers of B cells than the t-mock/t-CD40L control.

15

To further distinguish between viability and cellular proliferation, ³H-thymidine incorporation was also assessed on day 3. As expected, t-CD40L induced significant B cell proliferation, whereas neither t-mock nor t-CD100 induced significant proliferation. Proliferation induced by the combination of t-CD100/t-CD40L was not significantly greater than that observed with t-CD40L/t-mock demonstrating that the effect of CD100 signaling
20 is likely to be on viability rather than on proliferation.

Example 6: CD100 stimulation of B cells reduces CD40L induced increase in CD23 expression

This example shows that in addition to synergizing with CD40L in inducing B cell
25 clustering, CD100 modifies CD40L signaling by reducing CD23 induction induced by CD40L.

A two-color FACS analysis of human splenic B cells was performed after 72 hours of co-culture with t-mock/t-CD40L cells or t-CD100/t-CD40L. Cells were stained with CD19 conjugated to phycoerythrin and CD23 conjugated to fluorescein isothiocyanate
30 (Coulter, Hialeah, FL). Non-viable cells were excluded by propidium iodide counterstaining prior to analysis.

As shown in Figure 8, the percentage of CD23+CD19+ cells is consistently reduced (50-90% reduction) when the CD40L signal is delivered in the presence of CD100. In contrast, CD100 does not modify the induction of B7 family costimulatory molecules.
35 These results indicate that the CD100 signal not only amplifies the CD40L viability signal but also modifies the CD40L differentiative signal and therefore is likely to be important for the generation, organization, and/or regulation of B cells within the germinal center.

- 61 -

Example 7: CD100 stimulates T cell proliferation

The previous examples demonstrated that CD100 stimulating B cells to aggregate, extends their lifespan, and reduces the expression of CD23. This example demonstrates that CD100 can also provide a costimulatory signal to T cells.

5 5×10^4 CD4+ T cells were cultured in media, with an anti-CD3 antibody at 1 μ g/ml, with an anti-CD3 antibody at 1 μ g/ml and 2×10^4 NIH-3T3 cells transfected with B7-1 (t-B7-1), with an anti-CD3 antibody at 1 μ g/ml and 2×10^4 NIH-3T3 cells transfected with B7-2 (t-B7-2), or with an anti-CD3 antibody at 1 μ g/ml and 2×10^4 t-CD100 cells. 3 H-thymidine incorporation was assessed on day 3.

10 The results are shown in Figure 9. The results indicate that, similarly to t-B7-1 and t-B7-2, t-CD100 stimulate the proliferation of CD4+ T cells. Thus, these results indicate that CD100 is capable of stimulating the proliferation of T cells in the presence of a primary activation signal.

In another example the costimulatory effect of various amounts of t-CD100 cells on
15 CD4+ T cells was assessed. 5×10^4 CD4+ T cells were incubated with 1 μ g/ml anti-CD3 antibody, 2×10^4 t-B7-1 cells and 0, 1×10^4 , 2×10^4 , or 3×10^4 t-CD100 cells or t-B7-1 cells. 3 H-thymidine incorporation was assessed on day 3. The results, which are presented in Figure 10, indicate that the level of T cell proliferation increases progressively with increasing amounts of t-CD100 cells. The level of T cell proliferation obtained by
20 incubating T cells with a mixture of t-B7-1 and t-CD100 cells is similar to the level of T cell proliferation obtained by incubating T cells with t-CD100.

In a similar experiment, 5×10^4 CD4+ T cells were incubated with 1 μ g/ml anti-CD3 antibody, 2×10^4 t-B7-2 cells and 0, 1×10^4 , 2×10^4 , or 3×10^4 t-CD100 cells or t-B7-2 cells and thymidine incorporation was determined after 3 days of culture. The results,
25 shown in Figure 11, indicate that T cell proliferation increases progressively with increasing amounts of t-CD100 and t-B7-2 cells.

Thus, CD100 is capable of stimulating T cells to proliferate in the presence of a primary activation signal.

30 **Example 8: Cloning of a cDNA encoding murine CD100 and characterization of murine CD100**

This Example describes the isolation of a cDNA encoding a murine CD100 (mCD100) molecule and characteristics of mouse CD100 protein.

A cDNA library prepared from murine T cells activated with anti-CD3 and anti-
35 CD28 antibodies was screened with a probe corresponding to a nucleic acid encoding the sema and Ig domains of the human CD100 protein. The hybridization was carried out at 60° C under low stringency conditions (in the absence of formamide) with a final wash at 55° C in 2 x SSC, 0.1% SDS. More than 40 cDNA clones were obtained. One of these

- 62 -

clones contained an insert having the nucleic acid sequence SEQ ID NO: 8 shown in Figure 12 which encodes the full length mouse CD100 protein.

Northern blot hybridization using mCD100 cDNA indicated the presence of a 5.1 kb murine CD100 RNA in the Balb/c B lymphoma cell line A20. No mCD100 RNA was detected in L929 fibroblast cells and Chinese Hamster Ovary (CHO) cells.

Southern blot analysis of mouse genomic DNA with mCD100 cDNA indicated that the exons of the mCD100 gene are compactly organized. Only a single major band was evident after HindIII digestion along with 4 minor bands that might be small exons or other semaphorin gene family members. Three bands were observed after BamHI or EcoRI digestion.

Nucleic acid and amino acid sequence comparisons indicated that human and mouse CD100 are highly similar. Figure 13 shows a nucleic acid sequence comparison between mouse CD100 cDNA (SEQ ID NO: 8) and the open reading frame of human CD100 (SEQ ID NO: 22). This comparison shows that the open reading frame of human and mouse CD100 cDNA have 2141 out of 2586 nucleotides that are identical. Thus, mouse and human CD100 open reading frame nucleotide sequences have 83% homology or similarity.

A comparison between the amino acid sequence of human and mouse CD100 proteins indicated that the structural features of mouse CD100 (SEQ ID NO: 10) are similar to those of human CD100 protein (SEQ ID NO: 2). Similarly to human CD100, mouse CD100 protein has a signal, sema, Ig, stalk, transmembrane, and cytoplasmic domain, which are all highly conserved between mouse and human CD100. Mouse CD100 protein has a signal sequence from about amino acid 1 to about amino acid 22 or 24 of amino acid sequence shown in Figure 16 (SEQ ID NO: 9), a sema domain from about amino acid 42 to about amino acid 553 of amino acid sequence shown in Figure 14 (SEQ ID NO: 9), an Ig domain from about amino acid 554 or 566 to about amino acid 630 of amino acid sequence shown in Figure 14 (SEQ ID NO: 9), a stalk domain from about amino acid 631 to about amino acid 732 of amino acid sequence shown in Figure 14 (SEQ ID NO: 9), a transmembrane domain from about amino acid 734 to about amino acid 752 of amino acid sequence shown in Figure 14 (SEQ ID NO: 9), and a cytoplasmic domain from about amino acid 753 to about amino acid 861.

A comparison of the amino acid sequences of each domain of human and mouse CD100 proteins is shown in Figure 15 and the percentage homology between each domain is indicated in Table I. In this comparison, the domains are considered as having the following portions of the protein: signal peptide domain corresponding to amino acids 1-41 in mouse and human CD100; sema domain corresponding to amino acids 42-553 in mouse and human CD100; Ig-like domain corresponding to amino acids 554-630 in mouse and human CD100; stalk domain corresponding to amino acids 631-732 in mouse CD100 and amino acids 631-733 in human CD100; transmembrane domain corresponding to amino acids 734-752 in mouse CD100 and to amino acids 735-752 in human CD100; and

- 63 -

cytoplasmic domain corresponding to amino acids 753-861 in mouse CD100 and amino acids 754 to 862 in human CD100. The signal peptide, Sema domain, Ig domain, transmembrane (TM) domain and cytoplasmic domains of each protein have the same number of amino acids. The stalk domain of human CD100 is one amino acid (aa) longer than that of mouse CD100.

Table I
CD100, mouse/human comparison

Domain	# Identical aa	# Conserved aa	Total aa	% Identity
Signal	28	8	41	68%
Sema	454	19	512	88%
Ig	65	5	77	84%
Stalk	73	10	m103 or h104	70%
TM	16	1	19	84%
Cyto	102	4	109	94%
Total	738	47	m861 h862	86%

Table I indicates that among the protein domains, the cytoplasmic domain was most conserved, having 93% identity between the human and mouse domain. This is indicative of an important signaling function of the cytoplasmic (cyto) domain. The Sema domain is also highly conserved, having 454 amino acids out of 512 amino acids which are identical between mouse and human, corresponding to 88% identity. Most of the amino acid differences in the sema domain are in the COOH end. The stalk region tethering the Sema and Ig domains to the membrane was least conserved at 70% identity. Overall, mouse and human CD100 have 86% amino acid identity and 91% similarity (i.e., if conservative amino acid substitutions are allowed).

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

- 64 -
SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Hall, Kathryn T. et al.

(ii) TITLE OF INVENTION: CD100 Antigen and Uses Therefor

10

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

15

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- (E) COUNTRY: USA
- (F) ZIP: 02109-1875

20

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

30

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/556,422
- (B) FILING DATE: 09-NOV-1995

35

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45

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 88..2674

- 65 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	CTGAGCCGCA TCTGCAATAG CACACTTGCC CGGCCACCTG CTGCCGTGAG CCTTTGCTGC	60
	TGAAGCCCCT GGGGTCGCCT CTACCTG ATG AGG ATG TGC ACC CCC ATT AGG	111
	Met Arg Met Cys Thr Pro Ile Arg	
	1 5	
10	GGG CTG CTC ATG GCC CTT GCA GTG ATG TTT GGG ACA GCG ATG GCA TTT	159
	Gly Leu Leu Met Ala Leu Ala Val Met Phe Gly Thr Ala Met Ala Phe	
	10 15 20	
15	GCA CCC ATA CCC CGG ATC ACC TGG GAG CAC AGA GAG GTG CAC CTG GTG	207
	Ala Pro Ile Pro Arg Ile Thr Trp Glu His Arg Glu Val His Leu Val	
	25 30 35 40	
20	CAG TTT CAT GAG CCA GAC ATC TAC AAC TAC TCA GCC TTG CTG CTG AGC	255
	Gln Phe His Glu Pro Asp Ile Tyr Asn Tyr Ser Ala Leu Leu Leu Ser	
	45 50 55	
25	GAG GAC AAG GAC ACC TTG TAC ATA GGT GCC CGG GAG GCG GTC TTC GCT	303
	Glu Asp Lys Asp Thr Leu Tyr Ile Gly Ala Arg Glu Ala Val Phe Ala	
	60 65 70	
30	GTG AAC GCA CTC AAC ATC TCC GAG AAG CAG CAT GAG GTG TAT TGG AAG	351
	Val Asn Ala Leu Asn Ile Ser Glu Lys Gln His Glu Val Tyr Trp Lys	
	75 80 85	
35	GTC TCA GAA GAC AAA AAA GCA AAA TGT GCA GAA AAG GGG AAA TCA AAA	399
	Val Ser Glu Asp Lys Lys Ala Lys Cys Ala Glu Lys Gly Lys Ser Lys	
	90 95 100	
40	CAG ACA GAG TGC CTC AAC TAC ATC CGG GTG CTG CAG CCA CTC AGC GCC	447
	Gln Thr Glu Cys Leu Asn Tyr Ile Arg Val Leu Gln Pro Leu Ser Ala	
	105 110 115 120	
45	ACT TCC CTT TAC GTG TGT GGG ACC AAC GCA TTC CAG CCG GCC TGT GAC	495
	Thr Ser Leu Tyr Val Cys Gly Thr Asn Ala Phe Gln Pro Ala Cys Asp	
	125 130 135	
50	CAC CTG AAC TTA ACA TCC TTT AAG TTT CTG GGG AAA AAT GAA GAT GGC	543
	His Leu Asn Leu Thr Ser Phe Lys Phe Leu Gly Lys Asn Glu Asp Gly	
	140 145 150	
55	AAA GGA AGA TGT CCC TTT GAC CCA GCA CAC AGC TAC ACA TCC GTC ATG	591
	Lys Gly Arg Cys Pro Phe Asp Pro Ala His Ser Tyr Thr Ser Val Met	
	155 160 165	
60	GTT GAT GGA GAA CTT TAT TCG GGG ACG TCG TAT AAT TTT TTG GGA AGT	639
	Val Asp Gly Glu Leu Tyr Ser Gly Thr Ser Tyr Asn Phe Leu Gly Ser	
	170 175 180	
65	GAA CCC ATC ATC TCC CGA AAT TCT TCC CAC AGT CCT CTG AGG ACA GAA	687
	Glu Pro Ile Ile Ser Arg Asn Ser Ser His Ser Pro Leu Arg Thr Glu	
	185 190 195 200	

- 66 -

5	TAT GCA ATC CCT TGG CTG AAC GAG CCT AGT TTC GTG TTT GCT GAC GTG Tyr Ala Ile Pro Trp Leu Asn Glu Pro Ser Phe Val Phe Ala Asp Val	735
	205 210 215	
10	ATC CGA AAA AGC CCA GAC AGC CCC GAC GGC GAG GAT GAC AGG GTC TAC Ile Arg Lys Ser Pro Asp Ser Pro Asp Gly Glu Asp Asp Arg Val Tyr	783
	220 225 230	
15	TTC TTC TTC ACG GAG GTG TCT GTG GAG TAT GAG TTT GTG TTC AGG GTG Phe Phe Phe Thr Glu Val Ser Val Glu Tyr Glu Phe Val Phe Arg Val	831
	235 240 245	
20	CTG ATC CCA CGG ATA GCA AGA GTG TGC AAG GGG GAC CAG GGC GGC CTG Leu Ile Pro Arg Ile Ala Arg Val Cys Lys Gly Asp Gln Gly Gly Leu	879
	250 255 260	
25	AGG ACC TTG CAG AAG AAA TGG ACC TCC TTC CTG AAA GCC CGA CTC ATC Arg Thr Leu Gln Lys Lys Trp Thr Ser Phe Leu Lys Ala Arg Leu Ile	927
	265 270 275 280	
30	TGC TCC CGG CCA GAC AGC GGC TTG GTC TTC AAT GTG CTG CGG GAT GTC Cys Ser Arg Pro Asp Ser Gly Leu Val Phe Asn Val Leu Arg Asp Val	975
	285 290 295	
35	TTC GTG CTC AGG TCC CCG GGC CTG AAG GTG CCT GTG TTC TAT GCA CTC Phe Val Leu Arg Ser Pro Gly Leu Lys Val Pro Val Phe Tyr Ala Leu	1023
	300 305 310	
40	TTC ACC CCA CAG CTG AAC AAC GTG GGG CTG TCG GCA GTG TGC GCC TAC Phe Thr Pro Gln Leu Asn Asn Val Gly Leu Ser Ala Val Cys Ala Tyr	1071
	315 320 325	
45	AAC CTG TCC ACA GCC GAG GAG GTC TTC TCC CAC GGG AAG TAC ATG CAG Asn Leu Ser Thr Ala Glu Glu Val Phe Ser His Gly Lys Tyr Met Gln	1119
	330 335 340	
50	AGC ACC ACA GTG GAG CAG TCC CAC ACC AAG TGG GTG CGC TAT AAT GGC Ser Thr Thr Val Glu Gln Ser His Thr Lys Trp Val Arg Tyr Asn Gly	1167
	345 350 355 360	
55	CCG GTA CCC AAG CCG CGG CCT GGA GCG TGC ATC GAC AGC GAG GCA CGG Pro Val Pro Lys Pro Arg Pro Gly Ala Cys Ile Asp Ser Glu Ala Arg	1215
	365 370 375	
60	GCC GCC AAC TAC ACC AGC TCC TTG AAT TTG CCA GAC AAG ACG CTG CAG Ala Ala Asn Tyr Thr Ser Ser Leu Asn Leu Pro Asp Lys Thr Leu Gln	1263
	380 385 390	
65	TTC GTT AAA GAC CAC CCT TTG ATG GAT GAC TCG GTA ACC CCA ATA GAC Phe Val Lys Asp His Pro Leu Met Asp Asp Ser Val Thr Pro Ile Asp	1311
	395 400 405	
70	AAC AGG CCC AGG TTA ATC AAG AAA GAT GTG AAC TAC ACC CAG ATC GTG Asn Arg Pro Arg Leu Ile Lys Lys Asp Val Asn Tyr Thr Gln Ile Val	1359
	410 415 420	

- 67 -

	GTG	GAC	CGG	ACC	CAG	GCC	CTG	GAT	GGG	ACT	GTC	TAT	GAT	GTC	ATG	TTT	1407
	Val	Asp	Arg	Thr	Gln	Ala	Leu	Asp	Gly	Thr	Val	Tyr	Asp	Val	Met	Phe	
	425					430					435					440	
5	GTC	AGC	ACA	GAC	CGG	GGA	GCT	CTG	CAC	AAA	GCC	ATC	AGC	CTC	GAG	CAC	1455
	Val	Ser	Thr	Asp	Arg	Gly	Ala	Leu	His	Lys	Ala	Ile	Ser	Leu	Glu	His	
					445					450					455		
10	GCT	GTT	CAC	ATC	ATC	GAG	GAG	ACC	CAG	CTC	TTC	CAG	GAC	TTT	GAG	CCA	1503
	Ala	Val	His	Ile	Ile	Glu	Glu	Thr	Gln	Leu	Phe	Gln	Asp	Phe	Glu	Pro	
				460					465					470			
15	GTC	CAG	ACC	CTG	CTG	CTG	TCT	TCA	AAG	AAG	GGC	AAC	AGG	TTT	GTC	TAT	1551
	Val	Gln	Thr	Leu	Leu	Leu	Ser	Ser	Lys	Lys	Gly	Asn	Arg	Phe	Val	Tyr	
			475					480					485				
20	GCT	GGC	TCT	AAC	TCG	GGC	GTG	GTC	CAG	GCC	CCG	CTG	GCC	TTC	TGT	GGG	1599
	Ala	Gly	Ser	Asn	Ser	Gly	Val	Val	Gln	Ala	Pro	Leu	Ala	Phe	Cys	Gly	
	490					495					500						
25	AAG	CAC	GGC	ACC	TGC	GAG	GAC	TGT	GTG	CTG	GCG	CGG	GAC	CCC	TAC	TGC	1647
	Lys	His	Gly	Thr	Cys	Glu	Asp	Cys	Val	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	
	505				510						515					520	
30	GCC	TGG	AGC	CCG	CCC	ACA	GCG	ACC	TGC	GTG	GCT	CTG	CAC	CAG	ACC	GAG	1695
	Ala	Trp	Ser	Pro	Pro	Thr	Ala	Thr	Cys	Val	Ala	Leu	His	Gln	Thr	Glu	
				525					530					535			
35	AGC	CCC	AGC	AGG	GGT	TTG	ATT	CAG	GAG	ATG	AGC	GGC	GAT	GCT	TCT	GTG	1743
	Ser	Pro	Ser	Arg	Gly	Leu	Ile	Gln	Glu	Met	Ser	Gly	Asp	Ala	Ser	Val	
				540				545					550				
40	TGC	CCG	GAT	AAA	AGT	AAA	GGA	AGT	TAC	CGG	CAG	CAT	TTT	TTC	AAG	CAC	1791
	Cys	Pro	Asp	Lys	Ser	Lys	Gly	Ser	Tyr	Arg	Gln	His	Phe	Phe	Lys	His	
		555					560					565					
45	GGT	GGC	ACA	GCG	GAA	CTG	AAA	TGC	TCC	CAA	AAA	TCC	AAC	CTG	GCC	CGG	1839
	Gly	Gly	Thr	Ala	Glu	Leu	Lys	Cys	Ser	Gln	Lys	Ser	Asn	Leu	Ala	Arg	
	570					575					580						
50	GTC	TTT	TGG	AAG	TTC	CAG	AAT	GGC	GTG	TTG	AAG	GCC	GAG	AGC	CCC	AAG	1887
	Val	Phe	Trp	Lys	Phe	Gln	Asn	Gly	Val	Leu	Lys	Ala	Glu	Ser	Pro	Lys	
	585				590					595					600		
55	TAC	GGT	CTT	ATG	GGC	AGA	AAA	AAC	TTG	CTC	ATC	TTC	AAC	TTG	TCA	GAA	1935
	Tyr	Gly	Leu	Met	Gly	Arg	Lys	Asn	Leu	Leu	Ile	Phe	Asn	Leu	Ser	Glu	
				605				610				615					
60	GGA	GAC	AGT	GGG	GTG	TAC	CAG	TGC	CTG	TCA	GAG	GAG	AGG	GTT	AAG	AAC	1983
	Gly	Asp	Ser	Gly	Val	Tyr	Gln	Cys	Leu	Ser	Glu	Glu	Arg	Val	Lys	Asn	
			620					625				630					
65	AAA	ACG	GTC	TTC	CAA	GTG	GTC	GCC	AAG	CAC	GTC	CTG	GAA	GTG	AAG	GTG	2031
	Lys	Thr	Val	Phe	Gln	Val	Val	Ala	Lys	His	Val	Leu	Glu	Val	Lys	Val	
		635					640					645					

- 68 -

	GTT	CCA	AAG	CCC	GTA	GTG	GCC	CCC	ACC	TTG	TCA	GTT	GTT	CAG	ACA	GAA	2079
Val	Pro	Lys	Pro	Val	Val	Ala	Pro	Thr	Leu	Ser	Val	Val	Gln	Thr	Glu		
	650					655				660							
5	GGT	AGT	AGG	ATT	GCC	ACC	AAA	GTG	TTG	GTG	GCA	TCC	ACC	CAA	GGG	TCT	2127
	Gly	Ser	Arg	Ile	Ala	Thr	Lys	Val	Leu	Val	Ala	Ser	Thr	Gln	Gly	Ser	
	665				670					675					680		
	TCT	CCC	CCA	ACC	CCA	GCC	GTG	CAG	GCC	ACC	TCC	TCC	GGG	GCC	ATC	ACC	2175
10	Ser	Pro	Pro	Thr	Pro	Ala	Val	Gln	Ala	Thr	Ser	Ser	Gly	Ala	Ile	Thr	
					685					690					695		
	CTT	CCT	CCC	AAG	CCT	GCG	CCC	ACC	GGC	ACA	TCC	TGC	GAA	CCA	AAG	ATC	2223
15	Leu	Pro	Pro	Lys	Pro	Ala	Pro	Thr	Gly	Thr	Ser	Cys	Glu	Pro	Lys	Ile	
				700					705					710			
	GTC	ATC	AAC	ACG	GTC	CCC	CAG	CTC	CAC	TCG	GAG	AAA	ACC	ATG	TAT	CTT	2271
	Val	Ile	Asn	Thr	Val	Pro	Gln	Leu	His	Ser	Glu	Lys	Thr	Met	Tyr	Leu	
			715					720					725				
20	AAG	TCC	AGC	GAC	AAC	CGC	CTC	CTC	ATG	TCC	CTC	TTC	CTC	TTC	TTC	TTT	2319
	Lys	Ser	Ser	Asp	Asn	Arg	Leu	Leu	Met	Ser	Leu	Phe	Leu	Phe	Phe	Phe	
		730					735					740					
25	GTT	CTC	TTC	CTC	TGC	CTC	TTT	TTC	TAC	AAC	TGC	TAT	AAG	GGA	TAC	CTG	2367
	Val	Leu	Phe	Leu	Cys	Leu	Phe	Phe	Tyr	Asn	Cys	Tyr	Lys	Gly	Tyr	Leu	
		745				750					755					760	
	CCC	AGA	CAG	TGC	TTG	AAA	TTC	CGC	TCG	GCC	CTA	CTA	ATT	GGG	AAG	AAG	2415
30	Pro	Arg	Gln	Cys	Leu	Lys	Phe	Arg	Ser	Ala	Leu	Leu	Ile	Gly	Lys	Lys	
					765					770					775		
	AAG	CCC	AAG	TCA	GAT	TTC	TGT	GAC	CGT	GAG	CAG	AGC	CTG	AAG	GAG	ACG	2463
35	Lys	Pro	Lys	Ser	Asp	Phe	Cys	Asp	Arg	Glu	Gln	Ser	Leu	Lys	Glu	Thr	
				780					785					790			
	TTA	GTA	GAG	CCA	GGG	AGC	TTC	TCC	CAG	CAG	AAT	GGG	GAG	CAC	CCC	AAG	2511
	Leu	Val	Glu	Pro	Gly	Ser	Phe	Ser	Gln	Gln	Asn	Gly	Glu	His	Pro	Lys	
			795					800					805				
40	CCA	GCC	CTG	GAC	ACC	GGC	TAT	GAG	ACC	GAG	CAA	GAC	ACC	ATC	ACC	AGC	2559
	Pro	Ala	Leu	Asp	Thr	Gly	Tyr	Glu	Thr	Glu	Gln	Asp	Thr	Ile	Thr	Ser	
		810					815					820					
45	AAA	GTC	CCC	ACG	GAT	AGG	GAG	GAC	TCA	CAG	AGG	ATC	GAC	GAC	CTT	TCT	2607
	Lys	Val	Pro	Thr	Asp	Arg	Glu	Asp	Ser	Gln	Arg	Ile	Asp	Asp	Leu	Ser	
		825				830				835					840		
	GCC	AGG	GAC	AAG	CCC	TTT	GAC	GTC	AAG	TGT	GAG	CTG	AAG	TTC	GCT	GAC	2655
50	Ala	Arg	Asp	Lys	Pro	Phe	Asp	Val	Lys	Cys	Glu	Leu	Lys	Phe	Ala	Asp	
					8												

- 69 -

	CGTGCAAGTGC	TGCGTAGGTT	AGCCCGCATC	GTGCAGACAA	CCTCAGTCCT	CTTGTCTATT	2824
	TTCTCTTGGG	TTGAGCCTGT	GACTTGGTTT	CTCTTTGTCC	TTTGGAAAA	ATGACAAGCA	2884
5	TTGCATCCCA	GTCTTGTGTT	CCGAAGTCAG	TCGGAGTACT	TGAAGAAGGC	CCACGGGCGG	2944
	CACGGAGTTC	CTGAGCCCTT	TCTGTAGTGG	GGGAAAGGTG	GCTGGACCTC	TGTTGGCTGA	3004
	GAAGAGCATC	CCTTCAGCTT	CCCCTCCCCG	TAGCAGCCAC	TAAAAGATTA	TTTAATTCCA	3064
10	GATTGGAAAT	GACATTTTAG	TTTATCAGAT	TGTAACCTTA	TCGCCTGTTG	TCCAGATTGG	3124
	CACGAACCTT	TTCTTCCACT	TAATTATTTT	TTTAGGATTT	TGCTTTGATT	GTGTTTATGT	3184
15	CATGGGTCAT	TTTTTTTTTAG	TTACAGAAGC	AGTTGTGTTA	ATATTTAGAA	GAAGATGTAT	3244
	ATCTTCCAGA	TTTTGTTATA	TATTTGGCAT	AAAATACGGC	TTACGTTGCT	TAAGATTCTC	3304
	AGGGATAAAC	TTCCTTTTGC	TAAATGCATT	CTTCTGCTT	TTAGAAATGT	AGACATAAAC	3364
20	ACTCCCCGGA	GCCCACTCAC	CTTTTTTCTT	TTTCTTTTTT	TTTTTTTAAC	TTTATTCCTT	3424
	GAGGGAAGCA	TTGTTTTTGG	AGAGATTTTC	TTTCTGTACT	TCGTTTTACT	TTTCTTTTTT	3484
25	TTTAACTTTT	ACTCTCTCGA	AGAAGAGGAC	CTTCCCACAT	CCACGAGGTG	GGTTTTGAGC	3544
	AAGGGAAGGT	AGCCTGGATG	AGCTGAGTGG	AGCCAGGCTG	GCCCAGAGCT	GAGATGGGAG	3604
	TGCGGTACAA	TCTGGAGCCC	ACAGCTGTCT	GTCAGAACCT	CCTGTGAGAC	AGATGGAACC	3664
30	TTCACAAGGG	CGCCTTTGGT	TCTCTGAACA	TCTCCTTTCT	CTTCTTGCTT	CAATTGCTTA	3724
	CCCACTGCCT	GCCCAGACTT	TCTATCCAGC	CTCACTGAGC	TGCCCACTAC	TGGAAGGGAA	3784
35	CTGGGCCTCG	GTGGCCGGGG	CCGCGAGCTG	TGACCACAGC	ACCCTCAAGC	ATACGGCGCT	3844
	GTTCCCTGCCA	CTGTCCTGAA	GATGTGAATG	GGTGGTACGA	TTTCAACACT	GGTTAATTTT	3904
	ACACTCCATC	TCCCCGCTTT	GTAAATACCC	ATCGGGAAGA	GACTTTTTTTT	CCATGGTGAA	3964
40	GAGCAATAAA	CTCTGGATGT	TTGTGCGCGT	GTGTGGACAG	TCTTATCTTC	CAGCATGATA	4024
	GGATTTGACC	ATTTTGGTGT	AAACATTTGT	GTTTTATAAG	ATTTACCTTG	TTTTTATTTT	4084
45	TCTACTTTGA	ATTGTATACA	TTTGGAAGT	ACCCAAATAA	ATGAGAAGCT	TCTATCCTTA	4144
	AAAAAAAAAA	AAA					4157

50 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 862 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- 70 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Arg	Met	Cys	Thr	Pro	Ile	Arg	Gly	Leu	Leu	Met	Ala	Leu	Ala	Val	
	1				5					10					15		
5	Met	Phe	Gly	Thr	Ala	Met	Ala	Phe	Ala	Pro	Ile	Pro	Arg	Ile	Thr	Trp	
				20					25					30			
	Glu	His	Arg	Glu	Val	His	Leu	Val	Gln	Phe	His	Glu	Pro	Asp	Ile	Tyr	
10			35				40					45					
	Asn	Tyr	Ser	Ala	Leu	Leu	Leu	Ser	Glu	Asp	Lys	Asp	Thr	Leu	Tyr	Ile	
		50					55					60					
15	Gly	Ala	Arg	Glu	Ala	Val	Phe	Ala	Val	Asn	Ala	Leu	Asn	Ile	Ser	Glu	
	65				70					75					80		
	Lys	Gln	His	Glu	Val	Tyr	Trp	Lys	Val	Ser	Glu	Asp	Lys	Lys	Ala	Lys	
				85					90						95		
20	Cys	Ala	Glu	Lys	Gly	Lys	Ser	Lys	Gln	Thr	Glu	Cys	Leu	Asn	Tyr	Ile	
			100						105					110			
	Arg	Val	Leu	Gln	Pro	Leu	Ser	Ala	Thr	Ser	Leu	Tyr	Val	Cys	Gly	Thr	
25			115					120					125				
	Asn	Ala	Phe	Gln	Pro	Ala	Cys	Asp	His	Leu	Asn	Leu	Thr	Ser	Phe	Lys	
		130					135					140					
30	Phe	Leu	Gly	Lys	Asn	Glu	Asp	Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	
	145				150					155					160		
	Ala	His	Ser	Tyr	Thr	Ser	Val	Met	Val	Asp	Gly	Glu	Leu	Tyr	Ser	Gly	
				165					170					175			
35	Thr	Ser	Tyr	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Ile	Ser	Arg	Asn	Ser	
			180					185						190			
	Ser	His	Ser	Pro	Leu	Arg	Thr	Glu	Tyr	Ala	Ile	Pro	Trp	Leu	Asn	Glu	
40			195				200						205				
	Pro	Ser	Phe	Val	Phe	Ala	Asp	Val	Ile	Arg	Lys	Ser	Pro	Asp	Ser	Pro	
		210				215						220					
45	Asp	Gly	Glu	Asp	Asp	Arg	Val	Tyr	Phe	Phe	Phe	Thr	Glu	Val	Ser	Val	
	225				230						235				240		
	Glu	Tyr	Glu	Phe	Val	Phe	Arg	Val	Leu	Ile	Pro	Arg	Ile	Ala	Arg	Val	
				245					250					255			
50	Cys	Lys	Gly	Asp	Gln	Gly	Gly	Leu	Arg	Thr	Leu	Gln	Lys	Lys	Trp	Thr	
			260				265						270				
	Ser	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Arg	Pro	Asp	Ser	Gly	Leu	
55			275				280					285					
	Val	Phe	Asn	Val	Leu	Arg	Asp	Val	Phe	Val	Leu	Arg	Ser	Pro	Gly	Leu	
		290				295					300						

- 71 -

Lys Val Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val
 305 310 315 320

5 Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val
 325 330 335

Phe Ser His Gly Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His
 340 345 350

10 Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly
 355 360 365

15 Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu
 370 375 380

Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met
 385 390 395 400

20 Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Arg Leu Ile Lys Lys
 405 410 415

Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp
 420 425 430

25 Gly Thr Val Tyr Asp Val Met Phe Val Ser Thr Asp Arg Gly Ala Leu
 435 440 445

30 His Lys Ala Ile Ser Leu Glu His Ala Val His Ile Ile Glu Glu Thr
 450 455 460

Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu Leu Leu Ser Ser
 465 470 475 480

35 Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val
 485 490 495

Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu Asp Cys
 500 505 510

40 Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Pro Thr Ala Thr
 515 520 525

45 Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln
 530 535 540

Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser
 545 550 555 560

50 Tyr Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys
 565 570 575

Ser Gln Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly
 580 585 590

55 Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn
 595 600 605

- 72 -

Leu Leu Ile Phe Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys
 610 615 620
 Leu Ser Glu Glu Arg Val Lys Asn Lys Thr Val Phe Gln Val Val Ala
 5 625 630 635 640
 Lys His Val Leu Glu Val Lys Val Val Pro Lys Pro Val Val Ala Pro
 645 650 655
 10 Thr Leu Ser Val Val Gln Thr Glu Gly Ser Arg Ile Ala Thr Lys Val
 660 665 670
 Leu Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Val Gln
 15 675 680 685
 Ala Thr Ser Ser Gly Ala Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr
 690 695 700
 20 Gly Thr Ser Cys Glu Pro Lys Ile Val Ile Asn Thr Val Pro Gln Leu
 705 710 715 720
 His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu
 725 730 735
 25 Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu Cys Leu Phe Phe
 740 745 750
 Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg
 30 755 760 765
 Ser Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe Cys Asp
 770 775 780
 35 Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser
 785 790 795 800
 Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu
 805 810 815
 40 Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp
 820 825 830
 Ser Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val
 45 835 840 845
 Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
 850 855 860

50 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 655 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 73 -

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Trp	Leu	Thr	Arg	Ile	Val	Cys	Leu	Phe	Trp	Gly	Val	Leu	Leu	1	5	10	15
Thr	Ala	Arg	Ala	Asn	Tyr	Gln	Asn	Gly	Lys	Asn	Asn	Val	Pro	Arg	Leu	20	25	30	
Lys	Leu	Ser	Tyr	Lys	Glu	Met	Leu	Glu	Ser	Asn	Asn	Val	Ile	Thr	Phe	35	40	45	
Asn	Gly	Leu	Ala	Asn	Ser	Ser	Ser	Tyr	His	Thr	Phe	Leu	Leu	Asp	Glu	50	55	60	
Glu	Arg	Ser	Arg	Leu	Tyr	Val	Gly	Ala	Lys	Asp	His	Ile	Phe	Ser	Phe	65	70	75	80
Asp	Leu	Val	Asn	Ile	Lys	Asp	Phe	Gln	Lys	Ile	Val	Trp	Pro	Val	Ser	85	90	95	
Tyr	Thr	Arg	Arg	Asp	Glu	Cys	Lys	Trp	Ala	Gly	Lys	Asp	Ile	Leu	Lys	100	105	110	
Glu	Cys	Ala	Asn	Phe	Ile	Lys	Val	Leu	Lys	Ala	Tyr	Asn	Gln	Thr	His	115	120	125	
Leu	Tyr	Ala	Cys	Gly	Thr	Gly	Ala	Phe	His	Pro	Ile	Cys	Thr	Tyr	Ile	130	135	140	
Glu	Ile	Gly	His	His	Pro	Glu	Asp	Asn	Ile	Phe	Lys	Leu	Glu	Asn	Ser	145	150	155	160
His	Phe	Glu	Asn	Gly	Arg	Gly	Lys	Ser	Pro	Tyr	Asp	Pro	Lys	Leu	Leu	165	170	175	
Thr	Ala	Ser	Leu	Leu	Ile	Asp	Gly	Glu	Leu	Tyr	Ser	Gly	Thr	Ala	Ala	180	185	190	
Asp	Phe	Met	Gly	Arg	Asp	Phe	Ala	Ile	Phe	Arg	Thr	Leu	Gly	His	His	195	200	205	
His	Pro	Ile	Arg	Thr	Glu	Gln	His	Asp	Ser	Arg	Trp	Leu	Asn	Asp	Pro	210	215	220	
Lys	Phe	Ile	Ser	Ala	His	Leu	Ile	Ser	Glu	Ser	Asp	Asn	Pro	Glu	Asp	225	230	235	240
Asp	Lys	Val	Tyr	Phe	Phe	Phe	Arg	Glu	Asn	Ala	Ile	Asp	Gly	Glu	His	245	250	255	
Ser	Gly	Lys	Ala	Thr	His	Ala	Arg	Ile	Gly	Gln	Ile	Cys	Lys	Asn	Asp	260	265	270	

- 74 -

	Phe Gly Gly His Arg Ser Leu Val Asn Lys Trp Thr Thr Phe Leu Lys	275	280	285
5	Ala Arg Leu Ile Cys Ser Val Pro Gly Pro Asn Gly Ile Asp Thr His	290	295	300
	Phe Asp Glu Leu Gln Asp Val Phe Leu Met Asn Phe Lys Asp Pro Lys	305	310	315
10	Asn Pro Val Val Tyr Gly Val Phe Thr Thr Ser Ser Asn Ile Phe Lys	325	330	335
	Gly Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val Arg Arg Val Phe	340	345	350
15	Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr Gln Trp Val Pro	355	360	365
	Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys	370	375	380
20	Thr Phe Gly Gly Phe Asp Ser Thr Lys Asp Leu Pro Asp Asp Val Ile	385	390	395
	Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro Val Phe Pro Met	405	410	415
	Asn Asn Arg Pro Ile Val Ile Lys Thr Asp Val Asn Tyr Gln Phe Thr	420	425	430
30	Gln Ile Val Val Asp Arg Val Asp Ala Glu Asp Gly Gln Tyr Asp Val	435	440	445
	Met Phe Ile Gly Thr Asp Val Gly Thr Val Leu Lys Val Val Ser Ile	450	455	460
35	Pro Lys Glu Thr Trp Tyr Asp Leu Glu Glu Val Leu Leu Glu Glu Met	465	470	475
	Thr Val Phe Arg Glu Pro Thr Ala Ile Ser Ala Met Glu Leu Ser Thr	485	490	495
	Lys Gln Gln Gln Leu Tyr Ile Gly Ser Thr Ala Gly Val Ala Gln Leu	500	505	510
45	Pro Leu His Arg Cys Asp Ile Tyr Gly Lys Ala Cys Ala Glu Cys Cys	515	520	525
	Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp Gly Ser Ala Cys Ser Arg	530	535	540
50	Tyr Phe Pro Thr Ala Lys Arg Arg Thr Arg Arg Gln Asp Ile Arg Asn	545	550	555
	Gly Asp Pro Leu Thr His Cys Ser Asp Leu His His Asp Asn His His	565	570	575

- 75 -

Gly His Ser Pro Glu Glu Arg Ile Ile Tyr Gly Val Glu Asn Ser Ser
580 585 590

Thr Phe Leu Glu Cys Ser Pro Lys Ser Gln Arg Ala Leu Val Tyr Trp
5 595 600 605

Gln Phe Gln Arg Arg Asn Glu Glu Arg Lys Glu Glu Ile Arg Val Asp
610 615 620

10 Asp His Ile Ile Arg Thr Asp Gln Gly Leu Leu Leu Arg Ser Leu Gln
625 630 635 640

Gln Lys Asp Ser Gly Asn Tyr Leu Cys His Ala Val Glu His Gly
645 650 655

15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 607 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Glu Glu Arg Leu Ile Arg Lys Phe Glu Ala Glu Asn Ile Ser Asn Tyr
1 5 10 15

Thr Ala Leu Leu Leu Ser Gln Asp Gly Lys Thr Leu Tyr Val Gly Ala
35 20 25 30

Arg Glu Ala Leu Phe Ala Leu Asn Ser Asn Leu Ser Phe Leu Pro Gly
35 40 45

40 Gly Glu Tyr Gln Glu Leu Leu Trp Ser Ala Asp Ala Asp Arg Lys Gln
50 55 60

Gln Cys Ser Phe Lys Gly Lys Asp Pro Lys Arg Asp Cys Gln Asn Tyr
45 65 70 75 80

Ile Lys Ile Leu Leu Pro Leu Asn Ser Ser His Leu Leu Thr Cys Gly
85 90 95

Thr Ala Ala Phe Ser Pro Leu Cys Ala Tyr Ile His Ile Ala Ser Phe
50 100 105 110

Thr Leu Ala Gln Asp Glu Ala Gly Asn Val Ile Leu Glu Asp Gly Lys
115 120 125

55 Gly His Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala Leu Val Val
130 135 140

- 76 -

	Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe Gln Gly Asn Asp	
	145	155 160
5	Pro Ala Ile Ser Arg Ser Gln Ser Ser Arg Pro Thr Lys Thr Glu Ser	
	165	170 175
	Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe Val Ala Ser Ala Thr Ser	
	180	185 190
10	Pro Glu Ser Leu Gly Ser Pro Ile Gly Asp Asp Asp Lys Ile Tyr Phe	
	195	200 205
	Phe Phe Ser Glu Thr Gly Gln Glu Phe Glu Phe Phe Glu Asn Thr Ile	
	210	215 220
15	Val Ser Arg Val Ala Arg Val Cys Lys Gly Asp Glu Gly Gly Glu Arg	
	225	230 235 240
	Val Leu Gln Gln Arg Trp Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys	
20	245	250 255
	Ser Arg Pro Asp Asp Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe	
	260	265 270
25	Thr Leu Asn Pro Asn Pro Gln Asp Trp Arg Lys Thr Leu Ser Ile Gly	
	275	280 285
	Val Phe Thr Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Ile	
	290	295 300
30	Cys Val Phe Thr Met Asn Asp Val Gln Lys Ala Phe Asp Gly Leu Tyr	
	305	310 315 320
	Lys Lys Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Glu Thr His Gln	
35	325	330 335
	Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg Glu	
	340	345 350
40	Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu Asn Phe	
	355	360 365
	Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser Arg Leu Leu	
	370	375 380
45	Leu Leu Gln Pro Arg Ala Arg Tyr Gln Arg Val Ala Val His Arg Val	
	385	390 395 400
	Pro Gly Leu His Ser Thr Tyr Asp Val Leu Phe Leu Gly Thr Gly Asp	
50	405	410 415
	Gly Arg Leu His Lys Ala Val Thr Leu Ser Ser Arg Val His Ile Ile	
	420	425 430
55	Glu Glu Leu Gln Ile Phe Pro Gln Gly Gln Pro Val Gln Asn Leu Leu	
	435	440 445

- 77 -

Leu Asp Ser His Gly Gly Leu Leu Tyr Ala Ser Ser His Ser Gly Val
 450 455 460

Val Gln Val Pro Val Ala Asn Cys Ser Leu Tyr Pro Thr Cys Gly Asp
 465 470 475 480

Cys Leu Leu Ala Arg Asp Pro Tyr Cys Ala Trp Thr Gly Ser Ala Cys
 485 490 495

Arg Leu Ala Ser Leu Tyr Gln Pro Asp Leu Ala Ser Arg Pro Trp Thr
 500 505 510

Gln Asp Ile Glu Gly Ala Ser Val Lys Glu Leu Cys Lys Asn Ser Ser
 515 520 525

Tyr Lys Ala Arg Phe Leu Val Pro Gly Lys Pro Cys Lys Gln Val Gln
 530 535 540

Ile Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser Asn
 545 550 555 560

Leu Ala Thr Arg Leu Trp Val His Asn Gly Ala Pro Val Asn Ala Ser
 565 570 575

Ala Ser Cys Arg Val Leu Pro Thr Gly Asp Leu Leu Leu Val Gly Ser
 580 585 590

Gln Gln Gly Leu Gly Val Phe Gln Cys Trp Ser Ile Glu Glu Gly
 595 600 605

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Pro Ala Leu Asp Thr Gly Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

- 78 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Thr	Glu	Val	Ser	Val	Glu	Tyr	Glu	1	5	10	15
	Phe	Val	Gly	Lys	Leu	Met	Ile	Pro	Arg	Ile	Ala	Arg	Val	Cys	Lys	Arg	20	25	30	
10	Asp	Gln	Gly	Gly	Leu	Arg	Thr	Leu	Gln	Lys	Lys	Trp	Thr	Ser	Phe	Leu	35	40	45	
15	Lys	Ala	Arg	Leu	Ile	Cys	Thr	Ile	Pro	Asp	Lys	Asn	Leu	Ile	Phe	Asn	50	55	60	
	Ile	Ile	Asn	Asp	Val	Phe	Thr	Leu	Lys	Ser	Pro	Thr	Leu	Lys	Glu	Pro	65	70	75	80
20	Val	Ile	Tyr	Gly	Val	Phe	Thr	Pro	Gln	Leu	Asn	Asn	Val	Gly	Leu	Ser	85	90	95	
25	Ala	Val	Cys	Ala	Tyr	Asn	Leu	Ser	Ala	Val	Glu	Glu	Val	Phe	Ser	Lys	100	105	110	
	Gly	Lys	Tyr	Met	Gln	Ser	Ala	Thr	Val	Glu	Gln	Ser	His	Thr	Lys	Trp	115	120	125	
30	Val	Arg	Tyr	Asn	Gly	Glu	Ile	Pro	Asn	Pro	Arg	Pro	Gly	Ala	Cys	Ile	130	135	140	
	Asn	Asn	Glu	Ala	Arg	Ala	Leu	Asn	Tyr	Val	Thr	Ser	Leu	Asn	Leu	Pro	145	150	155	160
35	Asp	Lys	Thr	Leu	Gln	Phe	Val	Lys	Asp	His	Pro	Leu	Met	Asp	Asp	Ser	165	170	175	
40	Val	Thr	Pro	Val	Gly	Asp	Arg	Pro	Arg	Leu	Val	Lys	Arg	Asp	Val	Lys	180	185	190	
	Tyr	Thr	Gln	Ile	Val	Val	Asp	Arg	Val	Arg	Ala	Leu	Asn	Gly	Thr	Ile	195	200	205	
45	Tyr	Asp	Val	Met	Phe	Ile	Ser	Thr	Asp	Gln	Gly	Ala	Leu	His	Lys	Ala	210	215	220	
	Ile	Ser	Tyr	Glu	Asn	Gly	Met	His	Ile	Ile	Glu	Glu	Thr	Gln	Leu	Phe	225	230	235	240
50	Pro	Lys	Phe	Glu	Pro	Val	Gln	Thr	Leu	Leu	Leu	Ser	Ser	Lys	Lys	Ser	245	250	255	
55	Arg	Arg	Tyr	Leu	Tyr	Ala	Gly	Ser	Asn	Ser	Gly	Val	Val	Gln	Ser	Pro	260	265	270	
	Val	Ala	Phe	Cys	Asp	Thr	Tyr	Thr	Thr	Cys	Phe	Asp	Cys	Val	Leu	Ala	275	280	285	

- 79 -

Arg Asp Pro Tyr Cys Ala Trp
290 295

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 Gly Glu Leu Tyr Ser Gly Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro
1 5 10 15

Ile Ile Ser Arg Asn Ser Ser His Ser Pro Leu Arg Thr Glu Tyr Ala
20 25 30

25 Ile Pro Trp Leu Asn Glu Pro Ser Phe Val Phe Ala Asp Val Ile Arg
35 40 45

30 Lys Ser Pro Asp Ser Pro Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe
50 55 60

Phe Thr Glu Val Ser Val Glu Tyr Glu Phe Val Phe Arg Val Leu Ile
65 70 75 80

35 Pro Arg Ile Ala Arg Val Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr
85 90 95

40 Leu Gln Lys Lys Trp Thr Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser
100 105 110

Arg Pro Asp Ser Gly Leu Val Phe Asn Val Leu Arg Asp Val Phe Val
115 120 125

45 Leu Arg Ser Pro Gly Leu Lys Val Pro Val Phe Tyr Ala Leu Phe Thr
130 135 140

Pro Gln Leu Asn Asn Val Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu
145 150 155 160

50 Ser Thr Ala Glu Glu Val Phe Ser His Gly Lys Tyr Met Gln Ser Thr
165 170 175

Thr Val Glu Gln Ser His Thr Lys Trp Val Arg Tyr Asn Gly Pro Val
180 185 190

55 Pro Lys Pro Arg Pro Gly Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala
195 200 205

- 80 -

Asn Tyr Thr Ser Ser Leu Asn Leu Pro Asp Lys Thr Leu Gln Phe Val
 210 215 220
 Lys Asp His Pro Leu Met Asp Asp Ser Val Thr Pro Ile Asp Asn Arg
 225 230 235 240
 Pro Arg Leu Ile Lys Lys Asp Val Asn Tyr Thr Gln Ile Val Val Asp
 245 250 255
 Arg Thr Gln Ala Leu Asp Gly Thr Val Tyr Asp Val Met Phe Val Ser
 260 265 270
 Thr Asp Arg Gly Ala Leu His Lys Ala Ile Ser Leu Glu His Ala Val
 275 280 285
 His Ile Ile Glu Glu Thr Gln Leu Phe Gln Asp Phe Glu Pro Val Gln
 290 295 300
 Thr Leu Leu Leu Ser Ser Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly
 305 310 315 320
 Ser Asn Ser Gly Val Val Gln Ala Pro Leu Ala Phe Cys Gly Lys His
 325 330 335
 Gly Thr Cys Glu Asp Cys Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp
 340 345 350
 Ser Pro Pro Thr Ala Thr Cys Val Ala Leu His Gln Thr Glu Ser Pro
 355 360 365
 Ser Arg Gly Leu Ile Gln Glu Met Ser Gly Asp Ala Ser Val Cys Pro
 370 375 380
 Asp Lys Ser Lys Gly Ser Tyr Arg Gln His Phe Phe Lys His Gly Gly
 385 390 395 400
 Thr Ala Glu Leu Lys Cys Ser Gln Lys Ser Asn Leu Ala Arg Val Phe
 405 410 415
 Trp Lys Phe Gln Asn Gly Val Leu Lys
 420 425

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 434..3017

- 81 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	CATCTCCGCG CGTCTCCCGG CCTCCCCGAC TCAAGCTCCT GGCGCCGTTC GCCTCTGTCTG	60
5	TCGCTGCCAC CAACGCCGCC GCCATTCTTG GCGCGGAGCT GGCCTGGCCA GCCCCGCCC	120
	AGAGCCTCCG CGGGTCGGAC GCGCGCTCCA GACCCTGGTA ACACCACAGG AACACAGCCA	180
10	AGTCCTGAAT ACCGACATGT CTGACAGTGC TGATCCCTAG GTCAGACGGG AACACCGGCA	240
	GCCTTGGCAT GACGTCGTGA AGGTGGCCAT TGCTAACCTG ACATGTGGGG ACTCAGGAAC	300
	CCCACCCCTT ATGGGCTCCA GTCTGTGCTG CTGGCCCCAG CTCTGGGGCT CTAAGAGGTC	360
15	CTTGCTGCTA CCCCACAGCA GCCTGCTGCC ATCCATGTGT GCCCGTTGCT GAAGGCCTCG	420
	GTGGCCCCCTG CCC ATG AGG ATG TGT GCC CCC GTT AGG GGG CTG TTC TTG	469
	Met Arg Met Cys Ala Pro Val Arg Gly Leu Phe Leu	
20	1 5 10	
	GCC CTG GTG GTA GTG TTG AGA ACC GCG GTG GCA TTT GCA CCT GTG CCT	517
	Ala Leu Val Val Val Leu Arg Thr Ala Val Ala Phe Ala Pro Val Pro	
	15 20 25	
25	CGG CTC ACC TGG GAA CAT GGA GAG GTA GGT CTG GTG CAG TTT CAC AAG	565
	Arg Leu Thr Trp Glu His Gly Glu Val Gly Leu Val Gln Phe His Lys	
	30 35 40	
30	CCA GGC ATC TTT AAC TAC TCG GCC TTG CTG ATG AGT GAG GAC AAA GAC	613
	Pro Gly Ile Phe Asn Tyr Ser Ala Leu Leu Met Ser Glu Asp Lys Asp	
	45 50 55 60	
	ACT CTG TAT GTA GGC GCC CGG GAA GCA GTC TTT GCA GTG AAT GCG CTG	661
35	Thr Leu Tyr Val Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu	
	65 70 75	
	AAC ATC TCT GAG AAG CAA CAT GAG GTA TAT TGG AAG GTC TCT GAA GAC	709
	Asn Ile Ser Glu Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp	
40	80 85 90	
	AAA AAA TCC AAG TGT GCA GAG AAG GGG AAA TCA AAG CAG ACG GAA TGC	757
	Lys Lys Ser Lys Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys	
	95 100 105	
45	CTA AAC TAC ATT CGA GTA CTA CAG CCA CTA AGC AGC ACT TCC CTC TAT	805
	Leu Asn Tyr Ile Arg Val Leu Gln Pro Leu Ser Ser Thr Ser Leu Tyr	
	110 115 120	
50	GTG TGT GGG ACC AAT GCG TTC CAG CCC ACC TGT GAC CAC CTG AAC TTG	853
	Val Cys Gly Thr Asn Ala Phe Gln Pro Thr Cys Asp His Leu Asn Leu	
	125 130 135 140	
	ACA TCC TTC AAG TTT CTG GGG AAA AGT GAA GAT GGC AAA GGA AGA TGC	901
55	Thr Ser Phe Lys Phe Leu Gly Lys Ser Glu Asp Gly Lys Gly Arg Cys	
	145 150 155	

- 82 -

	CCC	TTC	GAC	CCC	GCC	CAC	AGC	TAC	ACA	TCA	GTC	ATG	GTT	GGG	GGC	GAG	949
	Pro	Phe	Asp	Pro	Ala	His	Ser	Tyr	Thr	Ser	Val	Met	Val	Gly	Gly	Glu	
				160					165					170			
5	CTC	TAC	TCT	GGG	ACG	TCC	TAT	AAT	TTC	TTG	GGC	AGT	GAA	CCC	ATC	ATC	997
	Leu	Tyr	Ser	Gly	Thr	Ser	Tyr	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Ile	
			175					180					185				
10	TCT	CGA	AAC	TCT	TCC	CAC	AGT	CCC	TTG	AGG	ACG	GAG	TAT	GCC	ATC	CCG	1045
	Ser	Arg	Asn	Ser	Ser	His	Ser	Pro	Leu	Arg	Thr	Glu	Tyr	Ala	Ile	Pro	
		190					195					200					
15	TGG	CTG	AAC	GAG	CCT	AGC	TTC	GTC	TTT	GCT	GAC	GTG	ATC	CAG	AAA	AGC	1093
	Trp	Leu	Asn	Glu	Pro	Ser	Phe	Val	Phe	Ala	Asp	Val	Ile	Gln	Lys	Ser	
	205					210					215					220	
20	CCA	GAT	GGT	CCG	GAG	GGT	GAA	GAT	GAC	AAG	GTC	TAC	TTC	TTT	TTT	ACG	1141
	Pro	Asp	Gly	Pro	Glu	Gly	Glu	Asp	Asp	Lys	Val	Tyr	Phe	Phe	Phe	Thr	
				225						230					235		
	GAG	GTA	TCC	GTG	GAG	TAC	GAA	TTC	GTC	TTC	AAG	TTG	ATG	ATC	CCG	CGA	1189
	Glu	Val	Ser	Val	Glu	Tyr	Glu	Phe	Val	Phe	Lys	Leu	Met	Ile	Pro	Arg	
			240					245						250			
25	GTT	GCC	AGG	GTG	TGC	AAG	GGC	GAC	CAG	GGC	GGC	CTG	CGG	ACT	TTG	CAA	1237
	Val	Ala	Arg	Val	Cys	Lys	Gly	Asp	Gln	Gly	Gly	Leu	Arg	Thr	Leu	Gln	
			255				260						265				
30	AAA	AAG	TGG	ACC	TCC	TTC	CTA	AAG	GCC	AGG	CTG	ATC	TGC	TCC	AAG	CCA	1285
	Lys	Lys	Trp	Thr	Ser	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Lys	Pro	
		270					275					280					
35	GAC	AGT	GGC	CTG	GTC	TTC	AAC	ATA	CTT	CAG	GAT	GTG	TTT	GTG	CTG	AGG	1333
	Asp	Ser	Gly	Leu	Val	Phe	Asn	Ile	Leu	Gln	Asp	Val	Phe	Val	Leu	Arg	
	285					290					295					300	
40	GCC	CCG	GGC	CTC	AAG	GAG	CCT	GTG	TTC	TAT	GCG	GTC	TTC	ACC	CCA	CAG	1381
	Ala	Pro	Gly	Leu	Lys	Glu	Pro	Val	Phe	Tyr	Ala	Val	Phe	Thr	Pro	Gln	
				305						310					315		
	CTG	AAC	AAT	GTG	GGT	CTG	TCA	GCG	GTG	TGC	GCC	TAC	ACA	CTG	GCC	ACG	1429
	Leu	Asn	Asn	Val	Gly	Leu	Ser	Ala	Val	Cys	Ala	Tyr	Thr	Leu	Ala	Thr	
				320					325					330			
45	GTG	GAG	GCA	GTC	TTC	TCC	CGT	GGA	AAG	TAC	ATG	CAG	AGT	GCC	ACA	GTG	1477
	Val	Glu	Ala	Val	Phe	Ser	Arg	Gly	Lys	Tyr	Met	Gln	Ser	Ala	Thr	Val	
			335					340					345				
50	GAG	CAG	TCT	CAC	ACC	AAG	TGG	GTG	CGC	TAC	AAT	GGC	CCA	GTG	CCC	ACT	1525
	Glu	Gln	Ser	His	Thr	Lys	Trp	Val	Arg	Tyr	Asn	Gly	Pro	Val	Pro	Thr	
		350					355					360					
55	CCC	CGA	CCT	GGA	GCG	TGT	ATC	GAC	AGT	GAG	GCC	CGG	GCA	GCC	AAC	TAC	1573
	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Asp	Ser	Glu	Ala	Arg	Ala	Ala	Asn	Tyr	
	365					370					375					380	

- 83 -

	ACC AGC TCC TTG AAT CTC CCA GAC AAA ACA CTG CAG TTT GTA AAA GAC	1621
	Thr Ser Ser Leu Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp	
	385 390 395	
5	CAC CCT TTG ATG GAT GAC TCA GTG ACC CCG ATA GAC AAC AGA CCC AAG	1669
	His Pro Leu Met Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Lys	
	400 405 410	
10	CTG ATC AAA AAA GAT GTA AAC TAC ACC CAG ATA GTG GTA GAC AGG ACC	1717
	Leu Ile Lys Lys Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr	
	415 420 425	
15	CAG GCC CTG GAT GGG ACT TTC TAC GAC GTC ATG TTC ATC AGC ACA GAC	1765
	Gln Ala Leu Asp Gly Thr Phe Tyr Asp Val Met Phe Ile Ser Thr Asp	
	430 435 440	
20	CGG GGA GCT CTG CAT AAA GCA GTC ATC CTC ACA AAA GAG GTG CAT GTC	1813
	Arg Gly Ala Leu His Lys Ala Val Ile Leu Thr Lys Glu Val His Val	
	445 450 455 460	
	ATC GAG GAG ACC CAA CTC TTC CGG GAC TCT GAA CCG GTC CTA ACT CTG	1861
	Ile Glu Glu Thr Gln Leu Phe Arg Asp Ser Glu Pro Val Leu Thr Leu	
	465 470 475	
25	CTG CTA TCG TCA AAG AAG GGG AGG AAG TTT GTC TAT GCA GGC TCC AAC	1909
	Leu Leu Ser Ser Lys Lys Gly Arg Lys Phe Val Tyr Ala Gly Ser Asn	
	480 485 490	
30	TCT GGA GTG GTC CAA GCG CCC CTG GCA TTC TGC GAA AAG CAC GGT AGC	1957
	Ser Gly Val Val Gln Ala Pro Leu Ala Phe Cys Glu Lys His Gly Ser	
	495 500 505	
35	TGT GAA GAC TGT GTG TTA GCA CGG GAC CCC TAC TGT GCC TGG AGC CCA	2005
	Cys Glu Asp Cys Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro	
	510 515 520	
40	GCC ATC AAG GCC TGT GTT ACC CTG CAC CAG GAA GAG GCC TCC AGC AGG	2053
	Ala Ile Lys Ala Cys Val Thr Leu His Gln Glu Glu Ala Ser Ser Arg	
	525 530 535 540	
	GGC TGG ATT CAG GAC ATG AGC GGT GAC ACA TCC TCA TGC CTG GAT AAG	2101
	Gly Trp Ile Gln Asp Met Ser Gly Asp Thr Ser Ser Cys Leu Asp Lys	
	545 550 555	
45	AGT AAA GAA AGT TTC AAC CAG CAT TTT TTC AAG CAC GGC GGC ACA GCG	2149
	Ser Lys Glu Ser Phe Asn Gln His Phe Phe Lys His Gly Gly Thr Ala	
	560 565 570	
50	GAA CTC AAA TGT TTC CAA AAG TCC AAC CTA GCC CGG GTG GTA TGG AAG	2197
	Glu Leu Lys Cys Phe Gln Lys Ser Asn Leu Ala Arg Val Val Trp Lys	
	575 580 585	
55	TTC CAG AAT GGC GAG TTG AAG GCC GCA AGT CCC AAG TAC GGC TTT GTG	2245
	Phe Gln Asn Gly Glu Leu Lys Ala Ala Ser Pro Lys Tyr Gly Phe Val	
	590 595 600	

- 84 -

	GGC	AGG	AAG	CAC	CTG	CTC	ATC	TTC	AAC	CTG	TCG	GAC	GGA	GAC	AGC	GGC	2293
	Gly	Arg	Lys	His	Leu	Leu	Ile	Phe	Asn	Leu	Ser	Asp	Gly	Asp	Ser	Gly	
	605					610					615					620	
5	GTG	TAC	CAG	TGC	CTG	TCA	GAG	GAA	AGG	GTG	AGG	AAT	AAA	ACG	GTC	TCC	2341
	Val	Tyr	Gln	Cys	Leu	Ser	Glu	Glu	Arg	Val	Arg	Asn	Lys	Thr	Val	Ser	
					625					630						635	
10	CAG	CTG	CTG	GCC	AAG	CAC	GTT	CTG	GAA	GTG	AAG	ATG	GTA	CCT	CGG	ACC	2389
	Gln	Leu	Leu	Ala	Lys	His	Val	Leu	Glu	Val	Lys	Met	Val	Pro	Arg	Thr	
				640					645						650		
15	CCC	CCC	TCA	CCT	ACC	TCA	GAG	GAT	GCT	CAG	ACA	GAA	GGT	AGT	AAG	ATC	2437
	Pro	Pro	Ser	Pro	Thr	Ser	Glu	Asp	Ala	Gln	Thr	Glu	Gly	Ser	Lys	Ile	
			655					660					665				
	ACA	TCC	AAA	ATG	CCG	GTT	GCA	TCT	ACC	CAG	GGG	TCC	TCT	CCC	CCT	ACC	2485
	Thr	Ser	Lys	Met	Pro	Val	Ala	Ser	Thr	Gln	Gly	Ser	Ser	Pro	Pro	Thr	
			670				675					680					
20	CCG	GCT	CTG	TGG	GCA	ACC	TCC	CCC	AGA	GCC	GCC	ACC	CTA	CCT	CCC	AAG	2533
	Pro	Ala	Leu	Trp	Ala	Thr	Ser	Pro	Arg	Ala	Ala	Thr	Leu	Pro	Pro	Lys	
	685					690					695					700	
25	TCC	TCC	TCC	GGC	ACA	TCC	TGT	GAA	CCA	AAG	ATG	GTC	ATC	AAC	ACG	GTC	2581
	Ser	Ser	Ser	Gly	Thr	Ser	Cys	Glu	Pro	Lys	Met	Val	Ile	Asn	Thr	Val	
				705						710					715		
30	CCC	CAG	CTC	CAC	TCA	GAG	AAG	ACG	GTG	TAT	CTC	AAG	TCC	AGT	GAC	AAC	2629
	Pro	Gln	Leu	His	Ser	Glu	Lys	Thr	Val	Tyr	Leu	Lys	Ser	Ser	Asp	Asn	
				720					725					730			
35	CGC	CTG	CTC	ATG	TCT	CTC	CTC	CTC	TTC	ATC	TTT	GTC	CTC	TTC	CTC	TGC	2677
	Arg	Leu	Leu	Met	Ser	Leu	Leu	Leu	Phe	Ile	Phe	Val	Leu	Phe	Leu	Cys	
			735					740					745				
	CTC	TTT	TCC	TAC	AAC	TGC	TAC	AAG	GGC	TAC	CTG	CCC	GGA	CAG	TGC	TTA	2725
	Leu	Phe	Ser	Tyr	Asn	Cys	Tyr	Lys	Gly	Tyr	Leu	Pro	Gly	Gln	Cys	Leu	
		750					755					760					
40	AAA	TTC	CGC	TCA	GCC	CTG	CTG	CTT	GGA	AAG	AAA	ACA	CCC	AAG	TCA	GAC	2773
	Lys	Phe	Arg	Ser	Ala	Leu	Leu	Gly	Lys	Lys	Thr	Pro	Lys	Ser	Asp		
		765				770				775					780		
45	TTC	TCT	GAC	CTG	GAG	CAG	AGT	GTG	AAG	GAG	ACA	CTG	GTC	GAG	CCT	GGG	2821
	Phe	Ser	Asp	Leu	Glu	Gln	Ser	Val	Lys	Glu	Thr	Leu	Val	Glu	Pro	Gly	
				785					790						795		
50	AGC	TTC	TCC	CAG	CAG	AAC	GGC	GAC	CAC	CCC	AAG	CCA	GCC	CTG	GAT	ACG	2869
	Ser	Phe	Ser	Gln	Gln	Asn	Gly	Asp	His	Pro	Lys	Pro	Ala	Leu	Asp	Thr	
				800				805						810			
55	GGC	TAT	GAA	ACG	GAG	CAG	GAC	ACC	ATC	ACC	AGC	AAA	GTC	CCC	ACG	GAT	2917
	Gly	Tyr	Glu	Thr	Glu	Gln	Asp	Thr	Ile	Thr	Ser	Lys	Val	Pro	Thr	Asp	
			815					820					825				

- 85 -

	CGT GAG GAC TCG CAA CGG ATC GAT GAA CTC TCT GCC CGG GAC AAA CCG	2965
	Arg Glu Asp Ser Gln Arg Ile Asp Glu Leu Ser Ala Arg Asp Lys Pro	
	830 835 840	
5	TTT GAT GTC AAG TGT GAA CTG AAG TTT GCA GAT TCG GAT GCT GAC GGG	3013
	Phe Asp Val Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly	
	845 850 855 860	
10	GAC T GAGGCCAGCG TGTCCCAGCC CATGCCCCCTC TGTCTTCGTG GAGAGTGTG	3067
	Asp *	
	TGTTGAGCCC ATTCAGTAGC CGAGTCTTGT CACTCTGTGC CAGCCTCAGT CCTGTGTCCC	3127
15	TTTTTCTCTT GGGTTGAGCC TGTGGCTCAT CCCCTTTGTC CTTTTGGGAA GCAAGTATCT	3187
	ATTCCAGTCT CAAGTCCTGC AGTTGCTGGA GCGCTTACGC ACCTGAGCCC TTTGTGTCTT	3247
20	GGGGGAGAGA TGGCCACCTC CGTGGGCTGC GAAGAGCCAC CCCTTCCTCT TCCGATTCTC	3307
	CTAGCAGCCA CTCAGAGATA ATTTAATTCC AGATTGGAAA CGCCCTTTTA GTTTATCAGA	3367
	TTGGTAACTT ACATCCTGCT GCCCAGATGG CACGGACAGT TTTCTTTTAC TTAATTATTA	3427
25	TTTTTTTTTT AAGGATTTTC GCTCCTATTG TGTTGATGTC TTAGGTCATT TTCTTTTTTT	3487
	CTTCTCTTT TTTTATTACC AGAGGAGATG TTTTAATATT CATGAGAAGA GGAACATTTT	3547
30	CTAGATTTTT TTGTTGTTAT ATATTGAGAT ATAAAATATG GCTATGTTGC TTAAGATTCT	3607
	CAGGGATAGA CTTATTTTTG TTAAC TTCAT TCTTCTCTGC TGTTAGGAAC ATAGGCCTAA	3667
	AATTGTCTCT TGAGTTTGCT CACCCTTTTG TTTTGGTAGG GTTTTTTTGT TGTTGCTGTT	3727
35	ATTGTTTCTA GTTTTAAATC TTATTCATTT TGAAGGATTT TTCTTTCTGA ACTTTTTTAA	3787
	TTTTTATATT TTCCTGCCAT ACATCTACAA AGTGGGTTTT GAGTGAGGGC AGGTGGCCCA	3847
40	GTGGCTTTGG GTGGCGACTG AGCTGGTCCC ACGAGGGGAG GAGGGTTTAT ATACCCCATG	3907
	ACCCTGCGGC TTCTTGCGGC CTCCTGCCCA TGAGGATCAC ATCCTGTCTC TCCTTGCTTC	3967
	CATCTCTCAT CACTGCCCTT GGACTTCCGC CTTGACTGTC CATGAAAGAC AGAAATGGGT	4027
45	TGGGTAGTTG GGCTCCCAAC CTCGGATGGT GACCGCAAAT CCCGGTGGGC GGCCGGCCGT	4087
	CTGCAGCCCC ATTCCTGCCA GTGTTTTTCTG GATGTAACGG GGGTACGATT TGGCATTGT	4147
50	TTTTCGCTCC CGGGTGGAAA TCATTCCATG TGGGGGACGA ATTTTGGATT CCCCCCACC	4207
	CCCACCCCGG CGGGTAGAAA TTTTTTTGCA TGACAGATTT ACCATTCGGT GTAAAATTTG	4267
	GTTTATAAGA TTTATTTGTT TTTATTTTTT TATGGACTGT AAATTTGAAA GTACCCAAAT	4327
55	AAACCGAGTT TTAATAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	4387
	AAAA	4391

- 86 -

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 861 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Arg Met Cys Ala Pro Val Arg Gly Leu Phe Leu Ala Leu Val Val
 1 5 10 15

15 Val Leu Arg Thr Ala Val Ala Phe Ala Pro Val Pro Arg Leu Thr Trp
 20 25 30

Glu His Gly Glu Val Gly Leu Val Gln Phe His Lys Pro Gly Ile Phe
 20 35 40 45

Asn Tyr Ser Ala Leu Leu Met Ser Glu Asp Lys Asp Thr Leu Tyr Val
 50 55 60

25 Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
 65 70 75 80

Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ser Lys
 85 90 95

30 Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
 100 105 110

Arg Val Leu Gln Pro Leu Ser Ser Thr Ser Leu Tyr Val Cys Gly Thr
 35 115 120 125

Asn Ala Phe Gln Pro Thr Cys Asp His Leu Asn Leu Thr Ser Phe Lys
 130 135 140

40 Phe Leu Gly Lys Ser Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro
 145 150 155 160

Ala His Ser Tyr Thr Ser Val Met Val Gly Gly Glu Leu Tyr Ser Gly
 165 170 175

45 Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser
 180 185 190

Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu
 50 195 200 205

Pro Ser Phe Val Phe Ala Asp Val Ile Gln Lys Ser Pro Asp Gly Pro
 210 215 220

55 Glu Gly Glu Asp Asp Lys Val Tyr Phe Phe Phe Thr Glu Val Ser Val
 225 230 235 240

- 87 -

	Glu Tyr Glu Phe Val Phe Lys Leu Met Ile Pro Arg Val Ala Arg Val	245	250	255
5	Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr	260	265	270
	Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Lys Pro Asp Ser Gly Leu	275	280	285
10	Val Phe Asn Ile Leu Gln Asp Val Phe Val Leu Arg Ala Pro Gly Leu	290	295	300
	Lys Glu Pro Val Phe Tyr Ala Val Phe Thr Pro Gln Leu Asn Asn Val	305	310	315
15	Gly Leu Ser Ala Val Cys Ala Tyr Thr Leu Ala Thr Val Glu Ala Val	325	330	335
	Phe Ser Arg Gly Lys Tyr Met Gln Ser Ala Thr Val Glu Gln Ser His	340	345	350
20	Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Thr Pro Arg Pro Gly	355	360	365
	Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu	370	375	380
	Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met	385	390	395
30	Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Lys Leu Ile Lys Lys	405	410	415
	Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp	420	425	430
35	Gly Thr Phe Tyr Asp Val Met Phe Ile Ser Thr Asp Arg Gly Ala Leu	435	440	445
	His Lys Ala Val Ile Leu Thr Lys Glu Val His Val Ile Glu Glu Thr	450	455	460
	Gln Leu Phe Arg Asp Ser Glu Pro Val Leu Thr Leu Leu Leu Ser Ser	465	470	475
45	Lys Lys Gly Arg Lys Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val	485	490	495
	Gln Ala Pro Leu Ala Phe Cys Glu Lys His Gly Ser Cys Glu Asp Cys	500	505	510
50	Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Ala Ile Lys Ala	515	520	525
	Cys Val Thr Leu His Gln Glu Glu Ala Ser Ser Arg Gly Trp Ile Gln	530	535	540

- 88 -

	Asp	Met	Ser	Gly	Asp	Thr	Ser	Ser	Cys	Leu	Asp	Lys	Ser	Lys	Glu	Ser	545	550	555	560
5	Phe	Asn	Gln	His	Phe	Phe	Lys	His	Gly	Gly	Thr	Ala	Glu	Leu	Lys	Cys	565	570	575	
	Phe	Gln	Lys	Ser	Asn	Leu	Ala	Arg	Val	Val	Trp	Lys	Phe	Gln	Asn	Gly	580	585	590	
10	Glu	Leu	Lys	Ala	Ala	Ser	Pro	Lys	Tyr	Gly	Phe	Val	Gly	Arg	Lys	His	595	600	605	
	Leu	Leu	Ile	Phe	Asn	Leu	Ser	Asp	Gly	Asp	Ser	Gly	Val	Tyr	Gln	Cys	610	615	620	
15	Leu	Ser	Glu	Glu	Arg	Val	Arg	Asn	Lys	Thr	Val	Ser	Gln	Leu	Leu	Ala	625	630	635	640
	Lys	His	Val	Leu	Glu	Val	Lys	Met	Val	Pro	Arg	Thr	Pro	Pro	Ser	Pro	645	650	655	
20	Thr	Ser	Glu	Asp	Ala	Gln	Thr	Glu	Gly	Ser	Lys	Ile	Thr	Ser	Lys	Met	660	665	670	
	Pro	Val	Ala	Ser	Thr	Gln	Gly	Ser	Ser	Pro	Pro	Thr	Pro	Ala	Leu	Trp	675	680	685	
	Ala	Thr	Ser	Pro	Arg	Ala	Ala	Thr	Leu	Pro	Pro	Lys	Ser	Ser	Ser	Gly	690	695	700	
30	Thr	Ser	Cys	Glu	Pro	Lys	Met	Val	Ile	Asn	Thr	Val	Pro	Gln	Leu	His	705	710	715	720
	Ser	Glu	Lys	Thr	Val	Tyr	Leu	Lys	Ser	Ser	Asp	Asn	Arg	Leu	Leu	Met	725	730	735	
35	Ser	Leu	Leu	Leu	Phe	Ile	Phe	Val	Leu	Phe	Leu	Cys	Leu	Phe	Ser	Tyr	740	745	750	
	Asn	Cys	Tyr	Lys	Gly	Tyr	Leu	Pro	Gly	Gln	Cys	Leu	Lys	Phe	Arg	Ser	755	760	765	
	Ala	Leu	Leu	Leu	Gly	Lys	Lys	Thr	Pro	Lys	Ser	Asp	Phe	Ser	Asp	Leu	770	775	780	
45	Glu	Gln	Ser	Val	Lys	Glu	Thr	Leu	Val	Glu	Pro	Gly	Ser	Phe	Ser	Gln	785	790	795	800
	Gln	Asn	Gly	Asp	His	Pro	Lys	Pro	Ala	Leu	Asp	Thr	Gly	Tyr	Glu	Thr	805	810	815	
50	Glu	Gln	Asp	Thr	Ile	Thr	Ser	Lys	Val	Pro	Thr	Asp	Arg	Glu	Asp	Ser	820	825	830	
	Gln	Arg	Ile	Asp	Glu	Leu	Ser	Ala	Arg	Asp	Lys	Pro	Phe	Asp	Val	Lys	835	840	845	

- 89 -

Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
 850 855 860

5 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

20 Met Arg Met Cys Ala Pro Val Arg Gly Leu Phe Leu Ala Leu Val Val
 1 5 10 15

Val Leu Arg Thr Ala Val Ala Phe Ala Pro Val Pro Arg Leu Thr Trp
 20 25 30

25

Glu His Gly Glu Val Gly Leu Val Gln
 35 40

30 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

45 Met Arg Met Cys Thr Pro Ile Arg Gly Leu Leu Met Ala Leu Ala Val
 1 5 10 15

Met Phe Gly Thr Ala Met Ala Phe Ala Pro Ile Pro Arg Ile Thr Trp
 20 25 30

50 Glu His Arg Glu Val His Leu Val Gln
 35 40

55

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- 90 -

(A) LENGTH: 512 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	Phe	His	Lys	Pro	Gly	Ile	Phe	Asn	Tyr	Ser	Ala	Leu	Leu	Met	Ser	Glu	
	1				5					10					15		
15	Asp	Lys	Asp	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Val	Phe	Ala	Val	
				20					25					30			
	Asn	Ala	Leu	Asn	Ile	Ser	Glu	Lys	Gln	His	Glu	Val	Tyr	Trp	Lys	Val	
			35					40					45				
20	Ser	Glu	Asp	Lys	Lys	Ser	Lys	Cys	Ala	Glu	Lys	Gly	Lys	Ser	Lys	Gln	
		50					55					60					
	Thr	Glu	Cys	Leu	Asn	Tyr	Ile	Arg	Val	Leu	Gln	Pro	Leu	Ser	Ser	Thr	
25	65					70					75					80	
	Ser	Leu	Tyr	Val	Cys	Gly	Thr	Asn	Ala	Phe	Gln	Pro	Thr	Cys	Asp	His	
				85						90					95		
30	Leu	Asn	Leu	Thr	Ser	Phe	Lys	Phe	Leu	Gly	Lys	Ser	Glu	Asp	Gly	Lys	
				100					105					110			
	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Ala	His	Ser	Tyr	Thr	Ser	Val	Met	Val	
			115					120					125				
35	Gly	Gly	Glu	Leu	Tyr	Ser	Gly	Thr	Ser	Tyr	Asn	Phe	Leu	Gly	Ser	Glu	
		130					135					140					
	Pro	Ile	Ile	Ser	Arg	Asn	Ser	Ser	His	Ser	Pro	Leu	Arg	Thr	Glu	Tyr	
40	145					150					155					160	
	Ala	Ile	Pro	Trp	Leu	Asn	Glu	Pro	Ser	Phe	Val	Phe	Ala	Asp	Val	Ile	
				165						170					175		
45	Gln	Lys	Ser	Pro	Asp	Gly	Pro	Glu	Gly	Glu	Asp	Asp	Lys	Val	Tyr	Phe	
				180				185						190			
	Phe	Phe	Thr	Glu	Val	Ser	Val	Glu	Tyr	Glu	Phe	Val	Phe	Lys	Leu	Met	
			195					200					205				
50	Ile	Pro	Arg	Val	Ala	Arg	Val	Cys	Lys	Gly	Asp	Gln	Gly	Gly	Leu	Arg	
		210					215					220					
	Thr	Leu	Gln	Lys	Lys	Trp	Thr	Ser	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	
55	225					230					235					240	
	Ser	Lys	Pro	Asp	Ser	Gly	Leu	Val	Phe	Asn	Ile	Leu	Gln	Asp	Val	Phe	
					245					250					255		

- 91 -

	Val	Leu	Arg	Ala	Pro	Gly	Leu	Lys	Glu	Pro	Val	Phe	Tyr	Ala	Val	Phe	
				260					265					270			
5	Thr	Pro	Gln	Leu	Asn	Asn	Val	Gly	Leu	Ser	Ala	Val	Cys	Ala	Tyr	Thr	
			275					280					285				
10	Leu	Ala	Thr	Val	Glu	Ala	Val	Phe	Ser	Arg	Gly	Lys	Tyr	Met	Gln	Ser	
		290						295				300					
	Ala	Thr	Val	Glu	Gln	Ser	His	Thr	Lys	Trp	Val	Arg	Tyr	Asn	Gly	Pro	
	305					310					315					320	
15	Val	Pro	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Asp	Ser	Glu	Ala	Arg	Ala	
					325					330					335		
	Ala	Asn	Tyr	Thr	Ser	Ser	Leu	Asn	Leu	Pro	Asp	Lys	Thr	Leu	Gln	Phe	
				340					345					350			
20	Val	Lys	Asp	His	Pro	Leu	Met	Asp	Asp	Ser	Val	Thr	Pro	Ile	Asp	Asn	
		355						360					365				
	Arg	Pro	Lys	Leu	Ile	Lys	Lys	Asp	Val	Asn	Tyr	Thr	Gln	Ile	Val	Val	
25		370				375						380					
	Asp	Arg	Thr	Gln	Ala	Leu	Asp	Gly	Thr	Phe	Tyr	Asp	Val	Met	Phe	Ile	
	385				390					395						400	
30	Ser	Thr	Asp	Arg	Gly	Ala	Leu	His	Lys	Ala	Val	Ile	Leu	Thr	Lys	Glu	
				405						410					415		
	Val	His	Val	Ile	Glu	Glu	Thr	Gln	Leu	Phe	Arg	Asp	Ser	Glu	Pro	Val	
			420					425						430			
35	Leu	Thr	Leu	Leu	Leu	Ser	Ser	Lys	Lys	Gly	Arg	Lys	Phe	Val	Tyr	Ala	
		435						440					445				
	Gly	Ser	Asn	Ser	Gly	Val	Val	Gln	Ala	Pro	Leu	Ala	Phe	Cys	Glu	Lys	
40		450					455					460					
	His	Gly	Ser	Cys	Glu	Asp	Cys	Val	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	
	465				470					475						480	
45	Trp	Ser	Pro	Ala	Ile	Lys	Ala	Cys	Val	Thr	Leu	His	Gln	Glu	Glu	Ala	
				485						490					495		
	Ser	Ser	Arg	Gly	Trp	Ile	Gln	Asp	Met	Ser	Gly	Asp	Thr	Ser	Ser	Cys	
50				500					505					510			

(2) INFORMATION FOR SEQ ID NO:13:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 512 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- 92 -

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 Phe His Glu Pro Asp Ile Tyr Asn Tyr Ser Ala Leu Leu Leu Ser Glu
 1 5 10 15
 Asp Lys Asp Thr Leu Tyr Ile Gly Ala Arg Glu Ala Val Phe Ala Val
 20 25 30
 15 Asn Ala Leu Asn Ile Ser Glu Lys Gln His Glu Val Tyr Trp Lys Val
 35 40 45
 20 Ser Glu Asp Lys Lys Ala Lys Cys Ala Glu Lys Gly Lys Ser Lys Gln
 50 55 60
 Thr Glu Cys Leu Asn Tyr Ile Arg Val Leu Gln Pro Leu Ser Ala Thr
 65 70 75 80
 25 Ser Leu Tyr Val Cys Gly Thr Asn Ala Phe Gln Pro Ala Cys Asp His
 85 90 95
 Leu Asn Leu Thr Ser Phe Lys Phe Leu Gly Lys Asn Glu Asp Gly Lys
 100 105 110
 30 Gly Arg Cys Pro Phe Asp Pro Ala His Ser Tyr Thr Ser Val Met Val
 115 120 125
 35 Asp Gly Glu Leu Tyr Ser Gly Thr Ser Tyr Asn Phe Leu Gly Ser Glu
 130 135 140
 Pro Ile Ile Ser Arg Asn Ser Ser His Ser Pro Leu Arg Thr Glu Tyr
 145 150 155 160
 40 Ala Ile Pro Trp Leu Asn Glu Pro Ser Phe Val Phe Ala Asp Val Ile
 165 170 175
 Arg Lys Ser Pro Asp Ser Pro Asp Gly Glu Asp Asp Arg Val Tyr Phe
 180 185 190
 45 Phe Phe Thr Glu Val Ser Val Glu Tyr Glu Phe Val Phe Arg Val Leu
 195 200 205
 50 Ile Pro Arg Ile Ala Arg Val Cys Lys Gly Asp Gln Gly Gly Leu Arg
 210 215 220
 Thr Leu Gln Lys Lys Trp Thr Ser Phe Leu Lys Ala Arg Leu Ile Cys
 225 230 235 240
 55 Ser Arg Pro Asp Ser Gly Leu Val Phe Asn Val Leu Arg Asp Val Phe
 245 250 255

- 93 -

	Val	Leu	Arg	Ser	Pro	Gly	Leu	Lys	Val	Pro	Val	Phe	Tyr	Ala	Leu	Phe	
					260				265						270		
5	Thr	Pro	Gln	Leu	Asn	Asn	Val	Gly	Leu	Ser	Ala	Val	Cys	Ala	Tyr	Asn	
			275					280					285				
	Leu	Ser	Thr	Ala	Glu	Glu	Val	Phe	Ser	His	Gly	Lys	Tyr	Met	Gln	Ser	
		290					295					300					
10	Thr	Thr	Val	Glu	Gln	Ser	His	Thr	Lys	Trp	Val	Arg	Tyr	Asn	Gly	Pro	
	305					310					315					320	
	Val	Pro	Lys	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Asp	Ser	Glu	Ala	Arg	Ala	
					325					330						335	
15	Ala	Asn	Tyr	Thr	Ser	Ser	Leu	Asn	Leu	Pro	Asp	Lys	Thr	Leu	Gln	Phe	
				340					345						350		
	Val	Lys	Asp	His	Pro	Leu	Met	Asp	Asp	Ser	Val	Thr	Pro	Ile	Asp	Asn	
20		355						360						365			
	Arg	Pro	Arg	Leu	Ile	Lys	Lys	Asp	Val	Asn	Tyr	Thr	Gln	Ile	Val	Val	
	370						375						380				
25	Asp	Arg	Thr	Gln	Ala	Leu	Asp	Gly	Thr	Val	Tyr	Asp	Val	Met	Phe	Val	
	385					390					395					400	
	Ser	Thr	Asp	Arg	Gly	Ala	Leu	His	Lys	Ala	Ile	Ser	Leu	Glu	His	Ala	
				405					410						415		
30	Val	His	Ile	Ile	Glu	Glu	Thr	Gln	Leu	Phe	Gln	Asp	Phe	Glu	Pro	Val	
			420					425						430			
	Gln	Thr	Leu	Leu	Leu	Ser	Ser	Lys	Lys	Gly	Asn	Arg	Phe	Val	Tyr	Ala	
35		435						440					445				
	Gly	Ser	Asn	Ser	Gly	Val	Val	Gln	Ala	Pro	Leu	Ala	Phe	Cys	Gly	Lys	
	450					455						460					
40	His	Gly	Thr	Cys	Glu	Asp	Cys	Val	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	
	465					470					475					480	
	Trp	Ser	Pro	Pro	Thr	Ala	Thr	Cys	Val	Ala	Leu	His	Gln	Thr	Glu	Ser	
				485					490						495		
45	Pro	Ser	Arg	Gly	Leu	Ile	Gln	Glu	Met	Ser	Gly	Asp	Ala	Ser	Val	Cys	
				500					505						510		

50 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- 94 -

(v) FRAGMENT TYPE: internal

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asp Lys Ser Lys Glu Ser Phe Asn Gln His Phe Phe Lys His Gly Gly
 1 5 10 15

10 Thr Ala Glu Leu Lys Cys Phe Gln Lys Ser Asn Leu Ala Arg Val Val
 20 25 30

Trp Lys Phe Gln Asn Gly Glu Leu Lys Ala Ala Ser Pro Lys Tyr Gly
 35 40 45

15 Phe Val Gly Arg Lys His Leu Leu Ile Phe Asn Leu Ser Asp Gly Asp
 50 55 60

20 Ser Gly Val Tyr Gln Cys Leu Ser Glu Glu Arg Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:15:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30 (v) FRAGMENT TYPE: internal

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Lys Ser Lys Gly Ser Tyr Arg Gln His Phe Phe Lys His Gly Gly
 1 5 10 15

40 Thr Ala Glu Leu Lys Cys Ser Gln Lys Ser Asn Leu Ala Arg Val Phe
 20 25 30

Trp Lys Phe Gln Asn Gly Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly
 35 40 45

45 Leu Met Gly Arg Lys Asn Leu Leu Ile Phe Asn Leu Ser Glu Gly Asp
 50 55 60

50 Ser Gly Val Tyr Gln Cys Leu Ser Glu Glu Arg Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:16:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- 95 -

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Arg Asn Lys Thr Val Ser Gln Leu Leu Ala Lys His Val Leu Glu Val
 1 5 10 15

10

Lys Met Val Pro Arg Thr Pro Pro Ser Pro Thr Ser Glu Asp Ala Gln
 20 25 30

15

Thr Glu Gly Ser Lys Ile Thr Ser Lys Met Pro Val Ala Ser Thr Gln
 35 40 45

Gly Ser Ser Pro Pro Thr Pro Ala Leu Trp Ala Thr Ser Pro Arg Ala
 50 55 60

20

Ala Thr Leu Pro Pro Lys Ser Ser Ser Gly Thr Ser Cys Glu Pro Lys
 65 70 75 80

Met Val Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Val Tyr
 85 90 95

25

Leu Lys Ser Ser Asp Asn
 100

(2) INFORMATION FOR SEQ ID NO:17:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Asn Lys Thr Val Phe Gln Val Val Ala Lys His Val Leu Glu Val
 1 5 10 15

45

Lys Val Val Pro Lys Pro Val Val Ala Pro Thr Leu Ser Val Val Gln
 20 25 30

50

Thr Glu Gly Ser Arg Ile Ala Thr Lys Val Leu Val Ala Ser Thr Gln
 35 40 45

Gly Ser Ser Pro Pro Thr Pro Ala Val Gln Ala Thr Ser Ser Gly Ala
 50 55 60

55

Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr Gly Thr Ser Cys Glu Pro
 65 70 75 80

- 96 -

Lys Ile Val Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Met
 85 90 95

5 Tyr Leu Lys Ser Ser Asp Asn
 100

(2) INFORMATION FOR SEQ ID NO:18:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Leu Met Ser Leu Leu Leu Phe Ile Phe Val Leu Phe Leu Cys Leu
 1 5 10 15

25 Phe Ser Tyr

(2) INFORMATION FOR SEQ ID NO:19:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Leu Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu Cys Leu
 1 5 10 15

45 Phe Phe Tyr

(2) INFORMATION FOR SEQ ID NO:20:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

- 97 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 Asn Cys Tyr Lys Gly Tyr Leu Pro Gly Gln Cys Leu Lys Phe Arg Ser
1 5 10 15

10 Ala Leu Leu Leu Gly Lys Lys Thr Pro Lys Ser Asp Phe Ser Asp Leu
20 25 30

Glu Gln Ser Val Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser Gln
35 40 45

15 Gln Asn Gly Asp His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu Thr
50 55 60

Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp Ser
20 65 70 75 80

Gln Arg Ile Asp Glu Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys
85 90 95

25 Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
100 105

(2) INFORMATION FOR SEQ ID NO:21:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg Ser
1 5 10 15

45 Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe Cys Asp Arg
20 25 30

Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser Gln
50 35 40 45

Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu Thr
50 55 60

55 Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp Ser
65 70 75 80

- 98 -

Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys
85 90 95

5 Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp
100 105

(2) INFORMATION FOR SEQ ID NO:22:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG AGG ATG TGC ACC CCC ATT AGG GGG CTG CTC ATG GCC CTT GCA GTG 48
Met Arg Met Cys Thr Pro Ile Arg Gly Leu Leu Met Ala Leu Ala Val
1 5 10 15

30 ATG TTT GGG ACA GCG ATG GCA TTT GCA CCC ATA CCC CGG ATC ACC TGG 96
Met Phe Gly Thr Ala Met Ala Phe Ala Pro Ile Pro Arg Ile Thr Trp
20 25 30

35 GAG CAC AGA GAG GTG CAC CTG GTG CAG TTT CAT GAG CCA GAC ATC TAC 144
Glu His Arg Glu Val His Leu Val Gln Phe His Glu Pro Asp Ile Tyr
35 40 45

AAC TAC TCA GCC TTG CTG CTG AGC GAG GAC AAG GAC ACC TTG TAC ATA 192
Asn Tyr Ser Ala Leu Leu Ser Glu Asp Lys Asp Thr Leu Tyr Ile
40 50 55 60

GGT GCC CGG GAG GCG GTC TTC GCT GTG AAC GCA CTC AAC ATC TCC GAG 240
Gly Ala Arg Glu Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu
65 70 75 80

AAG CAG CAT GAG GTG TAT TGG AAG GTC TCA GAA GAC AAA AAA GCA AAA 288
Lys Gln His Glu Val Tyr Trp Lys Val Ser Glu Asp Lys Lys Ala Lys
85 90 95

50 TGT GCA GAA AAG GGG AAA TCA AAA CAG ACA GAG TGC CTC AAC TAC ATC 336
Cys Ala Glu Lys Gly Lys Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile
100 105 110

55 CGG GTG CTG CAG CCA CTC AGC GCC ACT TCC CTT TAC GTG TGT GGG ACC 384
Arg Val Leu Gln Pro Leu Ser Ala Thr Ser Leu Tyr Val Cys Gly Thr
115 120 125

- 99 -

	AAC GCA TTC CAG CCG GCC TGT GAC CAC CTG AAC TTA ACA TCC TTT AAG	432
	Asn Ala Phe Gln Pro Ala Cys Asp His Leu Asn Leu Thr Ser Phe Lys	
	130 135 140	
5	TTT CTG GGG AAA AAT GAA GAT GGC AAA GGA AGA TGT CCC TTT GAC CCA	480
	Phe Leu Gly Lys Asn Glu Asp Gly Lys Gly Arg Cys Pro Phe Asp Pro	
	145 150 155 160	
10	GCA CAC AGC TAC ACA TCC GTC ATG GTT GAT GGA GAA CTT TAT TCG GGG	528
	Ala His Ser Tyr Thr Ser Val Met Val Asp Gly Glu Leu Tyr Ser Gly	
	165 170 175	
15	ACG TCG TAT AAT TTT TTG GGA AGT GAA CCC ATC ATC TCC CGA AAT TCT	576
	Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile Ile Ser Arg Asn Ser	
	180 185 190	
20	TCC CAC AGT CCT CTG AGG ACA GAA TAT GCA ATC CCT TGG CTG AAC GAG	624
	Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro Trp Leu Asn Glu	
	195 200 205	
25	CCT AGT TTC GTG TTT GCT GAC GTG ATC CGA AAA AGC CCA GAC AGC CCC	672
	Pro Ser Phe Val Phe Ala Asp Val Ile Arg Lys Ser Pro Asp Ser Pro	
	210 215 220	
30	GAC GGC GAG GAT GAC AGG GTC TAC TTC TTC TTC ACG GAG GTG TCT GTG	720
	Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe Phe Thr Glu Val Ser Val	
	225 230 235 240	
35	GAG TAT GAG TTT GTG TTC AGG GTG CTG ATC CCA CGG ATA GCA AGA GTG	768
	Glu Tyr Glu Phe Val Phe Arg Val Leu Ile Pro Arg Ile Ala Arg Val	
	245 250 255	
40	TGC AAG GGG GAC CAG GGC GGC CTG AGG ACC TTG CAG AAG AAA TGG ACC	816
	Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr	
	260 265 270	
45	TCC TTC CTG AAA GCC CGA CTC ATC TGC TCC CGG CCA GAC AGC GGC TTG	864
	Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Arg Pro Asp Ser Gly Leu	
	275 280 285	
50	GTC TTC AAT GTG CTG CGG GAT GTC TTC GTG CTC AGG TCC CCG GGC CTG	912
	Val Phe Asn Val Leu Arg Asp Val Phe Val Leu Arg Ser Pro Gly Leu	
	290 295 300	
55	AAG GTG CCT GTG TTC TAT GCA CTC TTC ACC CCA CAG CTG AAC AAC GTG	960
	Lys Val Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val	
	305 310 315 320	
60	GGG CTG TCG GCA GTG TGC GCC TAC AAC CTG TCC ACA GCC GAG GAG GTC	1008
	Gly Leu Ser Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val	
	325 330 335	
65	TTC TCC CAC GGG AAG TAC ATG CAG AGC ACC ACA GTG GAG CAG TCC CAC	1056
	Phe Ser His Gly Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His	
	340 345 350	

- 100 -

	ACC AAG TGG GTG CGC TAT AAT GGC CCG GTA CCC AAG CCG CGG CCT GGA	1104
	Thr Lys Trp Val Arg Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly	
	355 360 365	
5	GCG TGC ATC GAC AGC GAG GCA CGG GCC GCC AAC TAC ACC AGC TCC TTG	1152
	Ala Cys Ile Asp Ser Glu Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu	
	370 375 380	
10	AAT TTG CCA GAC AAG ACG CTG CAG TTC GTT AAA GAC CAC CCT TTG ATG	1200
	Asn Leu Pro Asp Lys Thr Leu Gln Phe Val Lys Asp His Pro Leu Met	
	385 390 395 400	
15	GAT GAC TCG GTA ACC CCA ATA GAC AAC AGG CCC AGG TTA ATC AAG AAA	1248
	Asp Asp Ser Val Thr Pro Ile Asp Asn Arg Pro Arg Leu Ile Lys Lys	
	405 410 415	
20	GAT GTG AAC TAC ACC CAG ATC GTG GTG GAC CGG ACC CAG GCC CTG GAT	1296
	Asp Val Asn Tyr Thr Gln Ile Val Val Asp Arg Thr Gln Ala Leu Asp	
	420 425 430	
25	GGG ACT GTC TAT GAT GTC ATG TTT GTC AGC ACA GAC CGG GGA GCT CTG	1344
	Gly Thr Val Tyr Asp Val Met Phe Val Ser Thr Asp Arg Gly Ala Leu	
	435 440 445	
30	CAC AAA GCC ATC AGC CTC GAG CAC GCT GTT CAC ATC ATC GAG GAG ACC	1392
	His Lys Ala Ile Ser Leu Glu His Ala Val His Ile Ile Glu Glu Thr	
	450 455 460	
35	CAG CTC TTC CAG GAC TTT GAG CCA GTC CAG ACC CTG CTG CTG TCT TCA	1440
	Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu Leu Leu Ser Ser	
	465 470 475 480	
40	AAG AAG GGC AAC AGG TTT GTC TAT GCT GGC TCT AAC TCG GGC GTG GTC	1488
	Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser Gly Val Val	
	485 490 495	
45	CAG GCC CCG CTG GCC TTC TGT GGG AAG CAC GGC ACC TGC GAG GAC TGT	1536
	Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu Asp Cys	
	500 505 510	
50	GTG CTG GCG CGG GAC CCC TAC TGC GCC TGG AGC CCG CCC ACA GCG ACC	1584
	Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Pro Thr Ala Thr	
	515 520 525	
55	TGC GTG GCT CTG CAC CAG ACC GAG AGC CCC AGC AGG GGT TTG ATT CAG	1632
	Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln	
	530 535 540	
60	GAG ATG AGC GGC GAT GCT TCT GTG TGC CCG GAT AAA AGT AAA GGA AGT	1680
	Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser	
	545 550 555 560	
65	TAC CGG CAG CAT TTT TTC AAG CAC GGT GGC ACA GCG GAA CTG AAA TGC	1728
	Tyr Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys	
	565 570 575	

- 101 -

	TCC CAA AAA TCC AAC CTG GCC CGG GTC TTT TGG AAG TTC CAG AAT GGC	1776
	Ser Gln Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly	
	580 585 590	
5	GTG TTG AAG GCC GAG AGC CCC AAG TAC GGT CTT ATG GGC AGA AAA AAC	1824
	Val Leu Lys Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn	
	595 600 605	
10	TTG CTC ATC TTC AAC TTG TCA GAA GGA GAC AGT GGG GTG TAC CAG TGC	1872
	Leu Leu Ile Phe Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys	
	610 615 620	
15	CTG TCA GAG GAG AGG GTT AAG AAC AAA ACG GTC TTC CAA GTG GTC GCC	1920
	Leu Ser Glu Glu Arg Val Lys Asn Lys Thr Val Phe Gln Val Val Ala	
	625 630 635 640	
20	AAG CAC GTC CTG GAA GTG AAG GTG GTT CCA AAG CCC GTA GTG GCC CCC	1968
	Lys His Val Leu Glu Val Lys Val Val Pro Lys Pro Val Val Ala Pro	
	645 650 655	
25	ACC TTG TCA GTT GTT CAG ACA GAA GGT AGT AGG ATT GCC ACC AAA GTG	2016
	Thr Leu Ser Val Val Gln Thr Glu Gly Ser Arg Ile Ala Thr Lys Val	
	660 665 670	
30	TTG GTG GCA TCC ACC CAA GGG TCT TCT CCC CCA ACC CCA GCC GTG CAG	2064
	Leu Val Ala Ser Thr Gln Gly Ser Ser Pro Pro Thr Pro Ala Val Gln	
	675 680 685	
35	GCC ACC TCC TCC GGG GCC ATC ACC CTT CCT CCC AAG CCT GCG CCC ACC	2112
	Ala Thr Ser Ser Gly Ala Ile Thr Leu Pro Pro Lys Pro Ala Pro Thr	
	690 695 700	
40	GGC ACA TCC TGC GAA CCA AAG ATC GTC ATC AAC ACG GTC CCC CAG CTC	2160
	Gly Thr Ser Cys Glu Pro Lys Ile Val Ile Asn Thr Val Pro Gln Leu	
	705 710 715 720	
45	CAC TCG GAG AAA ACC ATG TAT CTT AAG TCC AGC GAC AAC CGC CTC CTC	2208
	His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser Asp Asn Arg Leu Leu	
	725 730 735	
50	ATG TCC CTC TTC CTC TTC TTC TTT GTT CTC TTC CTC TGC CTC TTT TTC	2256
	Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu Cys Leu Phe Phe	
	740 745 750	
55	TAC AAC TGC TAT AAG GGA TAC CTG CCC AGA CAG TGC TTG AAA TTC CGC	2304
	Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu Lys Phe Arg	
	755 760 765	
60	TCG GCC CTA CTA ATT GGG AAG AAG AAG CCC AAG TCA GAT TTC TGT GAC	2352
	Ser Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe Cys Asp	
	770 775 780	
65	CGT GAG CAG AGC CTG AAG GAG ACG TTA GTA GAG CCA GGG AGC TTC TCC	2400
	Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe Ser	
	785 790 795 800	

- 102 -

	CAG CAG AAT GGG GAG CAC CCC AAG CCA GCC CTG GAC ACC GGC TAT GAG	2448
	Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu	
	805 810 815	
5	ACC GAG CAA GAC ACC ATC ACC AGC AAA GTC CCC ACG GAT AGG GAG GAC	2496
	Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp	
	820 825 830	
10	TCA CAG AGG ATC GAC GAC CTT TCT GCC AGG GAC AAG CCC TTT GAC GTC	2544
	Ser Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val	
	835 840 845	
15	AAG TGT GAG CTG AAG TTC GCT GAC TCA GAC GCA GAT GGA GAC	2586
	Lys Cys Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp	
	850 855 860	
	TGA	2589
	*	

- 103 -

CLAIMS

1. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a CD100 antigen.
- 5 2. The isolated nucleic acid molecule of claim 1, which is a cDNA.
3. The isolated nucleic acid molecule of claim 2, wherein the CD100 antigen is human.
- 10 4. The isolated nucleic acid of claim 3 comprising a nucleotide sequence shown in Figure 1, SEQ ID NO: 1.
5. The isolated nucleic acid of claim 4 comprising the coding region.
- 15 6. The isolated nucleic acid of claim 3 derived from a hematopoietic cell which hybridizes under high stringency conditions to a nucleic acid molecule comprising a nucleotide sequence shown in Figure 1, SEQ ID NO: 1.
- 20 7. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a protein wherein the protein comprises an amino acid sequence having at least about 80% overall amino acid sequence identity with an amino acid sequence shown in Figure 2, SEQ ID NO: 2.
- 25 8. The isolated nucleic acid molecule of claim 7, wherein the protein has a CD100 activity.
9. An isolated nucleic acid molecule encoding an amino acid sequence shown in Figure 2, SEQ ID NO: 2.
- 30 10. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a protein, wherein the protein comprises a semaphorin domain having an amino acid sequence at least 80% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2.
- 35 11. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a protein, wherein the protein comprises
 - a) a semaphorin domain having an amino acid sequence at least 60% identical to an amino acid sequence shown in Figure 2,

- 104 -

SEQ ID NO: 2; and

- b) an immunoglobulin-like domain having an amino acid sequence at least 50% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2.

5

12. The isolated nucleic acid molecule of claim 11, further comprising

- c) a cytoplasmic domain having an amino acid sequence at least 50% identical to an amino acid sequence shown in Figure 2, SEQ ID NO:

2.

10

13. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a protein, wherein the protein comprises an extracellular domain having an amino acid sequence at least 80% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2.

15

14. An isolated nucleic acid molecule encoding a CD100 fusion protein comprising a nucleotide sequence encoding a first peptide having an amino acid sequence at least 80% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2 and a nucleic sequence encoding a second peptide corresponding to a moiety that alters the solubility, binding affinity or valency of the first peptide.

20

15. The isolated nucleic acid molecule of claim 14, wherein the first peptide comprises an extracellular domain of a human CD100 antigen.

25

16. The isolated nucleic acid molecule of claim 14, wherein the first peptide comprises a semaphorin domain of a human CD100 antigen.

17. The isolated nucleic acid molecule of claim 14, wherein the second peptide comprises an immunoglobulin constant region.

30

18. An isolated nucleic acid molecule comprising a nucleotide sequence encoding a peptide comprising a fragment of at least about 30 amino acids of the sequence shown in Figure 2, SEQ ID NO: 2.

35

19. The isolated nucleic acid molecule of claim 18, wherein the peptide has a CD100 activity.

20. An isolated nucleic acid molecule of claim 1, which is antisense to the nucleic acid molecule of claim 1.

- 105 -

21. An isolated nucleic acid molecule of claim 1, which is antisense to the nucleic acid molecule of claim 4.
- 5 31. An isolated nucleic acid molecule of claim 1, which is antisense to the nucleic acid molecule of claim 5.
32. A vector comprising a nucleotide sequence encoding a CD100 antigen.
- 10 33. A vector comprising a nucleotide sequence encoding a protein comprising an amino acid sequence shown in Figure 2, SEQ ID NO: 2.
34. A host cell comprising the vector of claim 32.
- 15 35. A host cell comprising the vector of claim 33.
36. A method for producing a CD100 antigen comprising culturing a host cell of claim 34 in a suitable medium such that the CD100 antigen is produced.
- 20 37. A method for producing a CD100 antigen comprising culturing a host cell of claim 35 in a suitable medium such that the CD100 antigen is produced.
38. An isolated protein having a CD100 activity.
- 25 39. The isolated protein of claim 38, which is human.
40. The isolated protein of claim 39, wherein the protein comprises an amino acid sequence having at least about 80% overall amino acid sequence identity with an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).
- 30 41. The isolated protein of claim 40, wherein the protein comprises an amino acid sequence having at least about 90% overall amino acid sequence identity with an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).
- 35 42. The isolated protein of claim 40, wherein the protein comprises an amino acid sequence having at least about 95% overall amino acid sequence identity with an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).
43. The isolated protein of claim 39, wherein the protein has a CD100 activity.

- 106 -

44. The isolated protein of claim 43, which comprises an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).

5 45. An isolated protein comprising a semaphorin domain having an amino acid sequence at least 80% identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).

46. The isolated protein of claim 45 having an amino acid sequence at least 90% identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).

47. An isolated protein comprising

a) a semaphorin domain having an amino acid sequence at least 60% identical to an amino acid sequence shown in Figure 2

(SEQ ID NO: 2); and

b) an immunoglobulin-like domain having an amino acid sequence that is at least 50% identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).

48. The isolated protein of claim 47, further comprising

c) a cytoplasmic domain having an amino acid sequence at least 50% identical to an amino acid sequence shown in Figure 2 (SEQ ID NO: 2).

49. An isolated protein comprising an extracellular domain having an amino acid sequence at least 80% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2.

50. An CD100 fusion protein comprising a first peptide having an amino acid sequence at least 80% identical to an amino acid sequence shown in Figure 2, SEQ ID NO: 2 and a second peptide corresponding to a moiety that alters the solubility, binding affinity or valency of the first peptide.

51. The fusion protein of claim 50, wherein the first peptide comprises an extracellular domain of a human CD100 antigen.

52. The fusion protein of claim 50, wherein the first peptide comprises a semaphorin domain of a human CD100 antigen.

- 107 -

53. The fusion protein of claim 50, wherein the second peptide comprises an immunoglobulin constant region.
54. A peptide comprising a fragment of at least about 30 amino acids of the sequence
5 shown in Figure 2, SEQ ID NO: 2.
55. The peptide of claim 54, which has a CD100 activity.
56. The peptide of claim 54, wherein the fragment is at least about 40 amino acids in
10 length.
57. The peptide of claim 56, which has a CD100 activity.
58. The peptide of claim 56, wherein the fragment is at least about 50 amino acid in
15 length.
59. The peptide of claim 58, which has a CD100 activity.
60. A pharmaceutical composition comprising the protein of claim 44 and a
20 pharmaceutically acceptable carrier.
61. A pharmaceutical composition comprising the protein of claim 50 and a pharmaceutically acceptable carrier.
- 25 62. A pharmaceutical composition comprising the protein of claim 55 and a pharmaceutically acceptable carrier.
63. A vaccine composition comprising at least one antigen and a first agent which stimulates a CD100 ligand-associated signal.
30
64. The composition of claim 63, further comprising a second agent which stimulates a CD40-associated signal.
65. A method for modulating a B cell response comprising contacting the B cell with an
35 agent which modulates a CD100 ligand-associated signal in the B cell, such that a response by the B cell is modulated.
66. The method of claim 65, wherein the agent stimulates a CD100 ligand associated signal, such that a response by the B cell is stimulated.

- 108 -

67. The method of claim 66, wherein the agent is a stimulatory form of a CD100 antigen.

5 68. The method of claim 67, wherein the stimulatory form of a CD100 antigen is a soluble form of a CD100 antigen.

69. The method of claim 68, wherein the soluble form of a CD100 antigen is an immunoglobulin fusion protein.

10 70. The method of claim 67, wherein the stimulatory form of a CD100 antigen is attached to a solid phase support.

71. The method of claim 68, wherein the solid phase support is a cell membrane.

15 72. The method of claim 66, further comprising contacting the B cell with a second agent which provides a stimulatory signal to the B cell.

20 73. The method of claim 72, wherein the second agent stimulates a CD40 associated signal in the B cell.

74. The method of claim 73, wherein the second agent is a CD40 ligand.

75. The method of claim 66, further comprising contacting the B cells with T cells.

25 76. The method of claim 75, further comprising contacting the B cells with at least one antigen.

30 77. The method of claim 65, wherein the agent inhibits a CD100 ligand-associated signal, such that a response by the B cell is inhibited.

78. The method of claim 77, wherein the agent interacts with CD100.

79. The method of claim 78, wherein the agent is an antibody to CD100.

35 80. The method of claim 77, wherein the agent interacts with a CD100 ligand.

81. The method of claim 80, wherein the agent is an inhibitory form of CD100.

- 109 -

82. The method of claim 65, wherein the B cell response is B cell aggregation.

83. The method of claim 65, wherein the B cell response is B cell differentiation.

5 84. The method of claim 83, wherein the B cells differentiate into plasma cells.

85. The method of claim 83, wherein the B cells differentiate to memory B cells.

86. The method of claim 65, wherein the B cell response is B cell viability.

10

87. The method of claim 65, wherein contacting the cells is in a subject, such that a response by the B cell is modulated in the subject.

15 88. The method of claim 87, wherein the agent stimulates a B cell response in a subject infected with a pathogen, such that elimination of the pathogen by the subject is enhanced.

89. The method of claim 87, wherein the agent stimulates a B cell response in a subject having a low grade lymphoma, such that the B cell differentiation in the subject is stimulated.

20

90. The method of claim 88, further comprising administering to the subject a second agent which stimulates a CD40-associated signal in the B cell.

25 91. The method of claim 87, wherein the agent inhibits a B cell response in an allergic subject, such that the B cell response by the subject to an allergen is inhibited.

92. The method of claim 87, wherein the agent inhibits a B cell response in a subject having a large cell lymphoma, such that differentiation of the B cell in the subject is inhibited.

30

93. A method for modulating an interaction between an immune cell and a nerve cell in a subject, comprising administering to a subject an agent which modulates a CD100 ligand-associated signal in the nerve cell, such that modulation of the interaction between the immune cell and the nerve cell in the subject occurs.

35

94. A method for modulating axonal growth of a neuron, comprising contacting the neuron with a modulating form of CD100, such that axonal growth is modulated.

- 110 -

95. A method for modulating a T cell response, comprising contacting the T cell with an agent which modulates a CD100 ligand-induced signal in the T cell, such that a response in the T cell is modulated.

5 96. The method of claim 95, wherein a T cell is contacted with an agent which stimulates a CD100 ligand-induced signal in the T cell, such that a response in the T cell is stimulated.

10 97. The method of claim 96, further comprising contacting the T cell with an agent which provides a primary activation signal to the T cell.

98. The method of claim 95, wherein the T cell is contacted with an agent which inhibits a CD100 ligand-induced signal in the T cell, such that a response in the T cell is inhibited.

1/20

FIGURE 1

CD100 DNA and predicted protein sequence

		CTGAGCCGTCATCTGCAATAG	
1	21	CACACTTCCCCGCCACCTGCTGCCGTGAGCCTTTGCTGCTGAAGCCCTGGGGTCGCCTCTACCTG	17
		Met Arg Met Cys Thr Pro Ile Arg Gly Leu Leu Met Ala Leu Ala Val Met	
88	88	ATG AGG ATG TGC ACC CCC ATT AGG GGG CTG CTC ATG GCC CTT GCA GTG ATG	34
		Phe Gly Thr Ala Met Ala Phe Ala Pro Ile Pro Arg Ile Thr Trp Glu His	
139	139	TTT GGG ACA GCG ATG GCA TTT GCA CCC ATA CCC CGG ATC ACC TGG GAG CAC	51
		Arg Glu Val His Leu Val Gln Phe His Glu Pro Asp Ile Tyr Asn Tyr Ser	
190	190	AGA GAG GTG CAC CTG GTG CAG TTT CAT GAG CCA GAC ATC TAC AAC TAC TCA	68
		Ala Leu Leu Leu Ser Glu Asp Lys Asp Thr Leu Tyr Ile Gly Ala Arg Glu	
241	241	GCC TTG CTG CTG AGC GAG GAC AAG GAC ACC TTG TAC ATA GGT GCC CGG GAG	85
		Ala Val Phe Ala Val Asn Ala Leu Asn Ile Ser Glu Lys Gln His Glu Val	
292	292	GCG GTC TTC GCT GTG AAC GCA CTC AAC GCA AAA AAA GCA AAA TGT GCA GAA AAG GGG AAA	102
		Tyr Trp Lys Val Ser Glu Asp Lys Lys Ala Lys Cys Ala Glu Lys Gly Lys	
343	343	TAT TGG AAG GTC TCA GAA GAC AAA AAA GCA AAA TGT GCA GAA AAG GGG AAA	119
		Ser Lys Gln Thr Glu Cys Leu Asn Tyr Ile Arg Val Leu Gln Pro Leu Ser	
394	394	TCA AAA CAG ACA GAG TGC CTC AAC TAC ATC CGG GTG CTG CAG CCA CTC AGC	136
		Ala Thr Ser Leu Tyr Val Cys Gly Thr Asn Ala Phe Gln Pro Ala Cys Asp	
445	445	GCC ACT TCC CTT TAC CTG TGT GCG ACC AAC GCA TTC CAG CCG GCC TGT GAC	153
		His Leu Asn Leu Thr Ser Phe Lys Phe Leu Gly Lys Asn Glu Asp Gly Lys	
496	496	CAC CTG AAC TTA ACA TCC TTT AAG TTT CTG GGG AAA AAT GAA GAT GGC AAA	170
		Gly Arg Cys Pro Phe Asp Pro Ala His Ser Tyr Thr Ser Val Met Val Asp	
547	547	GGA AGA TGT CCC TTT GAG CCA GCA CAC AGC TAC ACA TCC GTC ATG GTT GAT	187
		Gly Glu Leu Tyr Ser Gly Thr Ser Tyr Asn Phe Leu Gly Ser Glu Pro Ile	
598	598	GGA GAA CTT TAT TCG GGG ACG TCG TAT AAT TTT TTG GGA AGT GAA CCC ATC	204
		Ile Ser Arg Asn Ser Ser His Ser Pro Leu Arg Thr Glu Tyr Ala Ile Pro	
649	649	ATC TCC CGA AAT TCT TCC CAC AGT CCT CTG AGG ACA GAA TAT GCA ATC CCT	221
		Trp Leu Asn Glu Pro Ser Phe Val Phe Val Phe Thr Glu Val	
700	700	TGG CTG AAC GAG CCT AGT TTC GTG TTT GCT GAC GTG ATC CGA AAA AGC CCA	238
		Asp Ser Pro Asp Gly Glu Asp Asp Arg Val Tyr Phe Phe Phe Thr Glu Val	
751	751	GAC AGC CCC GAC GGC GAG GAT GAC AGG GTC TAC TTC TTC TTC ACG GAG GTG	255
		Ser Val Glu Tyr Glu Phe Val Phe Arg Val Leu Ile Pro Arg Ile Ala Arg	
802	802	TCT GTG GAG TAT GAG TTT GTG TTC AGG CTG CTG ATC CCA CGG ATA GCA AGA	272
		Val Cys Lys Gly Asp Gln Gly Gly Leu Arg Thr Leu Gln Lys Lys Trp Thr	
853	853	GTG TCC AAG GGG GAC CAG GGC GGC CTG AGG ACC TTG CAG AAG AAA TGG ACC	289
		Ser Phe Leu Lys Ala Arg Leu Ile Cys Ser Arg Pro Asp Ser Gly Leu Val	
904	904	TCC TTC CTG AAA GCC CGA CTC ATT TTT TTT CCG CCA GAG AGC GGC TTG GTC	306
		Phe Asn Val Leu Arg Asp Val Phe Val Leu Arg Ser Pro Gly Leu Lys Val	
955	955	TTT AAT GTG CTG CCG GAT GTC TTC GTG CTC AGG TCC CCG GGC CTG AAG GTG	323
		Pro Val Phe Tyr Ala Leu Phe Thr Pro Gln Leu Asn Asn Val Gly Leu Ser	
1006	1006	CCT GTG TTC TAT GCA CTC TTC ACC CCA CAG CTG AAC AAC GTG GGC CTG TCG	340
		Ala Val Cys Ala Tyr Asn Leu Ser Thr Ala Glu Glu Val Phe Ser His Gly	
1057	1057	GCA GTG TGC GCC TAC AAC CTG TCC ACA GCC GAG GAG GTC TTC TCC CAC GGC	357
		Lys Tyr Met Gln Ser Thr Thr Val Glu Gln Ser His Thr Lys Trp Val Arg	
1108	1108	AAG TAC ATG CAG AGC ACC ACA GTG GAG CAG TCC CAC ACC AAG TGG GTG CGC	374
		Tyr Asn Gly Pro Val Pro Lys Pro Arg Pro Gly Ala Cys Ile Asp Ser Glu	
1159	1159	TAT AAT GGC CCG GTA CCC AAG CCG CCG CCT GGA GCG ATC GAC AGC GAG	391
		Ala Arg Ala Ala Asn Tyr Thr Ser Ser Leu Asn Leu Pro Asp Lys Thr Leu	
1210	1210	GCA CGG GCC GCC AAC TAC ACC AGC TCC TTG AAT TTG CCA GAC AAG ACG CTG	408
		Gln Phe Val Lys Asp His Pro Leu Met Asp Asp Ser Val Thr Pro Ile Asp	
1261	1261	CAG TTC GTT AAA GAC CAC CCT TTG ATG GAT GAC TCG GTA ACC CCA ATA GAC	425
		Asn Arg Pro Arg Leu Ile Lys Lys Asp Val Asn Tyr Thr Gln Ile Val Val	
1312	1312	AAC AGG CCC AGG TTA ATT AAG AAA GAT GAT GAT GAT GAT GAT GAT GAT GAT	442
		Asp Arg Thr Gln Ala Leu Asp Gly Thr Val Tyr Asp Val Met Phe Val Ser	
1363	1363	GAC CGG ACC CAG GCC CTG GAT GGG ATT GTC TAT GAT GTC ATG TTT GTC AGC	459
		Thr Asp Arg Gly Ala Leu His Lys Ala Ile Ser Leu Glu His Ala Val His	
1414	1414	ACA GAC CGG GGA GCT CTG CAC AAA GCC ATC AGC CTC GAG CAC GCT GTT CAC	476
		Ile Ile Glu Glu Thr Gln Leu Phe Gln Asp Phe Glu Pro Val Gln Thr Leu	
1465	1465	ATC ATC GAG GAG ACC CAG CTC CAG GAC TTT GAG CCA GTC CAG ACC CTG	493
		Leu Leu Ser Ser Lys Lys Gly Asn Arg Phe Val Tyr Ala Gly Ser Asn Ser	
1516	1516	CTG CTG TCT TCA AAG AAG GGC AAC AGG TTT GTC TAT GCT GGC TCT AAC TCG	510
		Gly Val Val Gln Ala Pro Leu Ala Phe Cys Gly Lys His Gly Thr Cys Glu	
1567	1567	GGC GTG GTC CAG GCC CCG CTG GCC TTC TGT GGG AAG CAC GGC ACC TGC GAG	527
		Asp Cys Val Leu Ala Arg Asp Pro Tyr Cys Ala Trp Ser Pro Thr Ala	
1618	1618	GAC TGT GTG CTG GCG CCG GAC CCC TAC TGC GCC TGG ACC CCG CCC ACA GCG	544
		Thr Cys Val Ala Leu His Gln Thr Glu Ser Pro Ser Arg Gly Leu Ile Gln	
1669	1669	ACC TGC GTG GCT CTG CAC CAG ACC GAG ACC CCC AGC AGC GGT TTG ATT CAG	561
		Glu Met Ser Gly Asp Ala Ser Val Cys Pro Asp Lys Ser Lys Gly Ser Tyr	
1720	1720	GAG ATG AGC GGC GAT GCT TCT GTG TGC CCG GAT AAA AGT AAA GGA AGT TAC	578
		Arg Gln His Phe Phe Lys His Gly Gly Thr Ala Glu Leu Lys Cys Ser Gln	
1771	1771	CGG CAG CAT TTT TTC AAG CAC GGT GGC ACA GCG GAA CTG AAA TGC TCC CAA	595
		Lys Ser Asn Leu Ala Arg Val Phe Trp Lys Phe Gln Asn Gly Val Leu Lys	
1822	1822	AAA TCC AAC CTG GCC CCG GTC TTT TGG AAG TTC CAG AAT GGC GTG TTG AAG	612
		Ala Glu Ser Pro Lys Tyr Gly Leu Met Gly Arg Lys Asn Leu Leu Ile Phe	
1873	1873	GCC GAG AGC CCC AAG TAC GGT CTT ATG GGC AGA AAA AAC TTG CTC ATC TTC	629
		Asn Leu Ser Glu Gly Asp Ser Gly Val Tyr Gln Cys Leu Ser Glu Glu Arg	
1924	1924	AAC TTG TCA GAA GGA GAC AGT GGG GTG TAC CAG TGC CTG TCA GAG GAG AGG	646
		Val Lys Asn Lys Thr Val Phe Gln Val Val Ala Lys His Val Leu Glu Val	
1975	1975	GTT AAG AAC AAA ACG GTC TTC CAA GTG GTC GCC AAG CAC GTC CTG GAA GTG	663
		Lys Val Val Pro Lys Pro Val Val Ala Pro Thr Leu Ser Val Val Gln Thr	
2026	2026	AAG GTG GTT CCA AAG CCC GTA GTG GCC CCC ACC TTG TCA GTT GTT CAG ACA	680
		Glu Gly Ser Arg Ile Ala Thr Lys Val Leu Val Ala Ser Thr Gln Gly Ser	

2/20

FIGURE 1 (CONTINUED)

2077 GAA GGT AGT AGG ATT GCC ACC AAA GTG TTG GTG GCA TCC ACC CAA GGG TCT
Ser Pro Pro Thr Pro Ala Val Gln Ala Thr Ser Ser Gly Ala Ile Thr Leu 697
2128 TCT CCC CCA ACC CCA GCC GTG CAG GGT ACC TTC TTC GGG GCC ATC ACC CTT
Pro Pro Lys Pro Ala Pro Thr Gly Thr Ser Cys Glu Pro Lys Ile Val Ile 714
2179 CCT CCC AAG CCT GCG CCC ACC GGC ACA TTC TGC GAA CCA AAG ATC GTC ATC
Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Met Tyr Leu Lys Ser Ser 731
2230 AAC ACG GTC CCC CAG CTC CAC TCG CAG AAA ACC ATG TAT CTT AAG TCC AGC
Asp Asn Arg Leu Leu Met Ser Leu Phe Leu Phe Phe Phe Val Leu Phe Leu 748
2281 GAC AAC CGC CTC CTC ATG TCC CTC TTC CTC TTC TTT GTT CTC CTC
Cys Leu Phe Phe Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro Arg Gln Cys Leu 765
2332 TGC CTC TTT TTC TAC AAC TGC TAT AAG GGA TAC CTG CCC AGA CAG TGC TTG
Lys Phe Arg Ser Ala Leu Leu Ile Gly Lys Lys Lys Pro Lys Ser Asp Phe 782
2383 AAA TTC CGC TCG GCC CTA CTA ATT GGG AAG AAG AAG CCC AAG TCA GAT TTC
Cys Asp Arg Glu Gln Ser Leu Lys Glu Thr Leu Val Glu Pro Gly Ser Phe 799
2434 TGT GAC CGT GAG CAG AGC CTG AAG GAG ACG TTA GTA GAG CCA GGG AGC TTC
Ser Gln Gln Asn Gly Glu His Pro Lys Pro Ala Leu Asp Thr Gly Tyr Glu 816
2485 TCC CAG CAG AAT GCG GAG CAC CCC AAG CCA GCC CTG GAC ACC GGC TAT GAG
Thr Glu Gln Asp Thr Ile Thr Ser Lys Val Pro Thr Asp Arg Glu Asp Ser 833
2536 ACC GAG CAA GAC ACC ATC ACC AGC AAA GTC CCC ACG GAT AGG GAG GAC TCA
Gln Arg Ile Asp Asp Leu Ser Ala Arg Asp Lys Pro Phe Asp Val Lys Cys 850
2587 CAG AGG ATC GAC GAC CTT TCT GCC AGG GAC AAG CCC TTT GAC GTC AAG TGT
Glu Leu Lys Phe Ala Asp Ser Asp Ala Asp Gly Asp Stop 862
2638 GAG CTG AAG TTC GCT GAC TCA GAC GCA GAT GGA GAC TGA GCGCGGCTGTGCATC
2692 CCGCTGGTGCCTCGGCTGGCAGCTGTCCAGGCGTGGAGAGTTTGTGTCTCTCTGTTTCAGTATCC
2759 GAGTCTCGTGCAGTGTGCGTAGGTTAGCCCGCATCGTGCAGACAACCTCAGTCTCTCTGTCTATTT
2826 TCTCTTGGGTTGAGCCGTGTGACTTGGTTTCTCTTTGTCTTTTGGAAAAATGACAAGCAATTGCATCC
2893 CAGTCTTGTGTTCCGAAGTCAGTCCGAGTACTTGAAGAAGGCCACGGGGCGGCACGGAGTTCTCTGAG
2960 CCTTTTCTGTAGTGGGGAAAGGTGGCTGGACCTCTGTGGCTGAGAAGAGCATCCCTTCAGCTTCC
3027 CCTCCCGTAGCAGCCACTAAAAGATTATTTAATCCAGATTGGAAATGACATTTTAGTTTATCAGA
3094 TTGGTAACTTATCGCCTGTGTCCAGATTGGCAGCAACCTTTTCTTCCACTTAATTATTTTTTAGG
3161 ATTTTGTCTTGATTGTGTTTATGTTCATGGGTCAATTTTTTTTAGTTACAGAAGCAGTTGTGTTAATA
3228 TTTAGAAGAAGATGTATATCTTCCAGATTTTGTATATATTTGGCATAAAATACGGCTTACGTTGCT
3295 TAAGATTCTCAGGGATAAACTTCCCTTTTGCTAAATGCATTTCTTCTGCTTTTAGAAAATGTAGACATA
3362 AACACTCCCCGGAGCCCACTCACCTTTTTCTTTTTCTTTTTTTTTTTAACTTTATTCCTTGAGG
3429 GAAGCATTTGTTTTTGGAGAGATTTCTTTCTCTACTTCTGTTTTACTTTCTTTTTTTTTTAACPTTTA
3496 CTCTCTCGAAGAAGAGGACCTTCCACATCTTAAGGTTGTTTTTGAACAAGGGAAGGTAGCCTGGA
3563 TGAGCTGAGTGGAGCCAGGCTGGTCCAGACTTGAATTTTACTTGGCTTACCAATCTGGAGCCCAAGC
3630 TGTCTGTCAGAACTTCTGTGTGAGACAGATGAAATTTTGAAGAAGGTTTCTGTTCTCTGAACATC
3697 TCCCTTCTCTTCTTCTTCAATTGCTTACCTTACTTGTGTTGCTGAGACTTTCTATCCAGCCTCACTGAG
3764 CTGCCCCACTACTGGAAGGGAAGTGGGCTCGGTGTCGAGGCGGAGGCTGTGACCACAGCACCCCTC
3831 AAGCATACGGCGCTGTTCTCTGCCACTGTCTCTGAAATGTGAATGGGTGTACGATTTCAACACTGGT
3898 TAATTTCACTCCATCTCCCCGCTTTGTAAATATCATGUGGCAAGAACTTTTTCATGGTGAA
3965 GAGCAATAAACTCTGGATGTTTGTGCGGCTGTGTGACAGTCTTATCTTCAGCATGATAGGATTTG
4032 ACCATTTTGGTGTAAACATTTGTGTTTTATAAGATTTACCTTGTTTTTATTTTTCTACTTTGAATTG
4099 TATACATTTGGAAAGTACCCAAATAAATGAGAAGCTTCTATCTTAAAAA

CD100 : MRMCTP RGL LMA LAVM FOTAMAFAP IPRITWEHRE V H LV 40
H-Serum M : MQWLTR I V CILFWGVLLTARANYONGKNNVPRKLKSYKEML 40
M-Serum C : EERLI 40

CD100 : Q - - - - - FHE - PDIIYNYS ALLLSEDKDTLYIGAREANFAN 73
H-Serum M : ESNNVITFNGLANSSSYHTFLLDEERERLYVGAKDHIFFS 73
M-Serum C : - - R - - - KFEA - ENISNYT ALLLSPDQKTLVGOAREALFAL 40

CD100 : NA - LN - - ISEKQHEVYMKVSEDKKAKCAEKQKS KQTECLN 110
H-Serum M : D - - - - LVNICKDFOKIVMPVSYIARDECKWAKDILKECIAN 110
M-Serum C : NSNLSFLPGGEYQELLWSADADRKOQCSFKQKDPKRDCCN 110

CD100 : YIRNLOPLSATSLYVCGTNAFDPACDHLNLT - - - - - FR 144
H-Serum M : FIKVLKAYNOITHLYACGTGAFFPICYIEIQHMPEDNIFK 144
M-Serum C : YIKTILPLNSHMLTCCGTAAFFPILCAYIHIA - - - - - FT 144

CD100 : FLQKN - - - - - EDGKQRCPFDPAHGYTSMVVDGELYSGTS 178
H-Serum M : LENS - - - - - FENGRQKSPYDPKLLTASLLIDGELYSGTA 178
M-Serum C : LAQDEAGNVILEDGKGHCFFDPNFKSTALVVDGELYTGT 178

CD100 : YNFLGSEPIISRNSHS - PLRTE - YAIPLWNEPSFVIFADV 218
H-Serum M : ADFMORPFAIFRTLGHHMHPITTEOHSERWLNOPKFTSAHL 218
M-Serum C : SSFOGNDPAISRSGSR - PTKTE - SSNLWLOPPAFVJASAT 192

CD100 : IRKSPDSPOQEDDRVYFFFTVSVYEYFNFVLIPIRIARV 258
H-Serum M : LSES - DNP - - EDDKVYFFFRNAIDQHSOKATHARIGD 258
M-Serum C : SPESLGSPICDDDKITVFFFSITGQEFEFENTIVSRVARV 258

CD100 : CKQDQGGGLRTLOKKWTSFLKARLICSRPD - SGLV - - FNVL 293
H-Serum M : CKNDIFQGHASLYNKWTFLKARLICSPVPPNGIDTHFDEL 293
M-Serum C : CKQDEGGGERVLOORWTSFLKARLICSRPD - DQFF - - FNVL 293

CD100 : RQVFVLR - - SPOLKVPVVFALFTPLNNVGL - - SAVCAYN 329
H-Serum M : ODVFLMNFKDF - - KNPVNYGVFTT - - SSNIFKSAVCMYS 329
M-Serum C : ODVETLNPPODWRKTLSTGVFTSDWHROTTESSATCVFT 329

CD100 : LSTAEVFSHGKYMOSTTVEQSHTKWVRNQPVPKPRPGA 369
H-Serum M : MSDVRRVFL - GPYAH - - - - - DGPNYQWVPYQORVPYPRPGT 369
M-Serum C : MNDVQKAF - DGLYKK - - - - - VNRETOQWYTETHOYPTPRPGA 369

CD100 : CIDSEARAANYTSSLNLPDKTLOFVKDHPLMDDSVTPIDN 409
H-Serum M : CFSKT - - FQGFDSIKDLPDDVLTFAHSPAMYNPMFPMNN 409
M-Serum C : CITNSABERKINSSELLOLPDRVNLFLKDHFLMDQ - - - - - OVR 382

CD100 : RPRLIKKQVNYT - - QIVVDRTQALDGTVYDVMFVSTDRGA 447
H-Serum M : RPJIVIKTDVNYQFTQIVVDRTQALDGTVYDVMFVSTDRGA 447
M-Serum C : RLLLLQPRARYO - - RYAVHHRVPLMST - - YDVLFLGTQDGR 447

CD100 : LHKALISLEHAV - - - - - HIEETDLFDDEFVOTLLSSK 481
H-Serum M : VLKMYSLPKETWYDLEEVLLLENTVFREPTAISAMELSTK 481
M-Serum C : LHKAVTUSRV - - - - - HIEETDLIFQGGQPVONLLLSM 481

CD100 : KQNRFFVYAGNSGVVQAPLAFCKHG - TCEDCVLARDPYC 520
H-Serum M : QOO - - - - - LYIGSTAGVADLP LHRCDIYGKACAECLARDPYC 520
M-Serum C : GQ - - - - - LLYASSMSGVVONPVANCSLYP - TCCDCVLARDPYC 520

CD100 : AWSPTATCVALHOTESPERGLIDEMSODA - - SVCPDKSK 558
H-Serum M : AWOGSAC - - - - - SYIEPTAKRRTRQDTRNGDPLTHCSOLNH 558
M-Serum C : AWTGSACRLASLYOPDLASRPWTODIEGASVKELCKN - - - 558

CD100 : GSYRQHF - - - - - - - - - - - FKHQGTAE - LKCSOKSNLARV 588
H-Serum M : DNHHGL - - - - - - - - - - - SPEERIIYOVENSSTIFLECSFKSORALV 588
M-Serum C : SYKARFLVPGPKQVO - - - - - IOPTVNT - LACFLLSNLATRL 588

CD100 : WKFO - - NGV LKAES - - PKYGLMQRKNLLIFNLSEODSGVY 623
H-Serum M : WQFORRNEERKEELRVDDHIRTDOGLLLRSLOPKDEGNY 623
M-Serum C : W - - VH - - - - - NGAPVNAS - - ASCRVLPQDLLLLVG - SOOGLGVF 623

CD100 : GCLSEERVKNKTYFOVVAKHVLEVKVVPKVVAPTLSVD 663
H-Serum M : LCHAVENG 663
M-Serum C : GCVSIEED 663

CD100 : 663 TEGSRIATKVLVASTOGSSPPTPAVQATSSGAITLPPKPA 703

CD100 : 703 PTQTSCEPKIVINTVPOLHSEKTMYLKSSDNRLMSLFLF 742

CD100 : 742 FFVFLCLFFYNCKYGYLPRODCLKFRSALLIGKKPKSDF 782

CD100 : 783 CDREOSLKETLVEPGSFSOONGEHPKPAIDTGYETEODTI 822

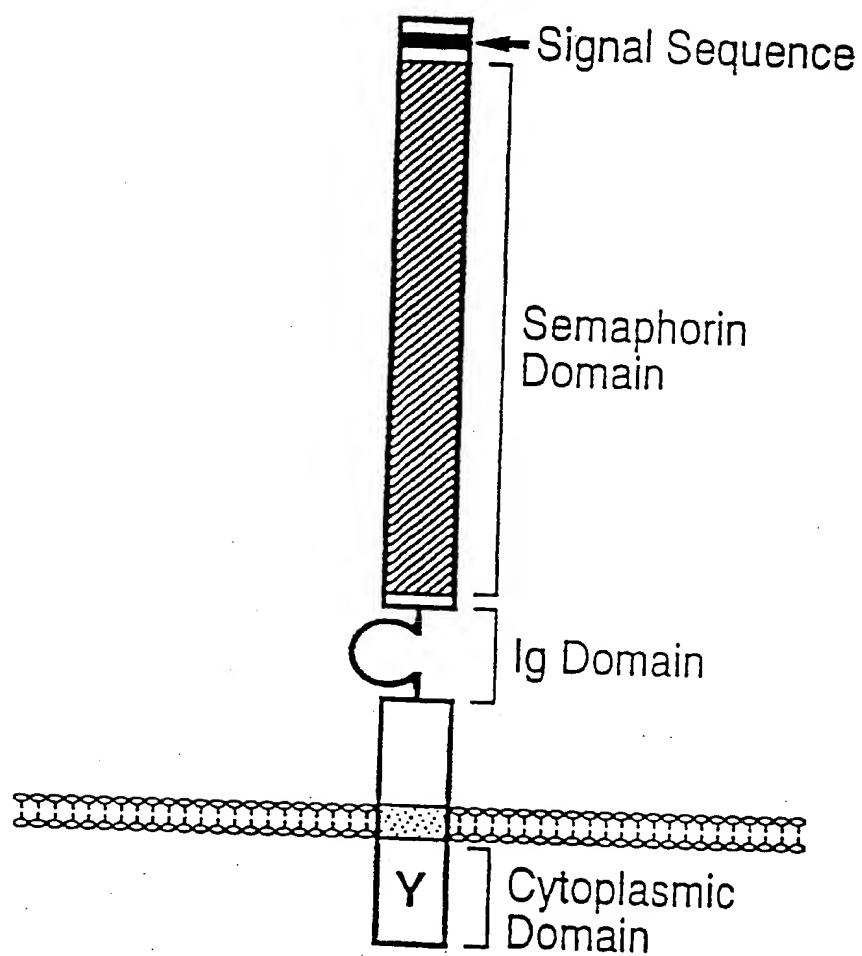
CD100 : 823 TSKVPTDREDSQRIDDLSARDKPFQVKCELKFADSDADGD 862

FIGURE 2

4/20

FIGURE 3

Human CD100



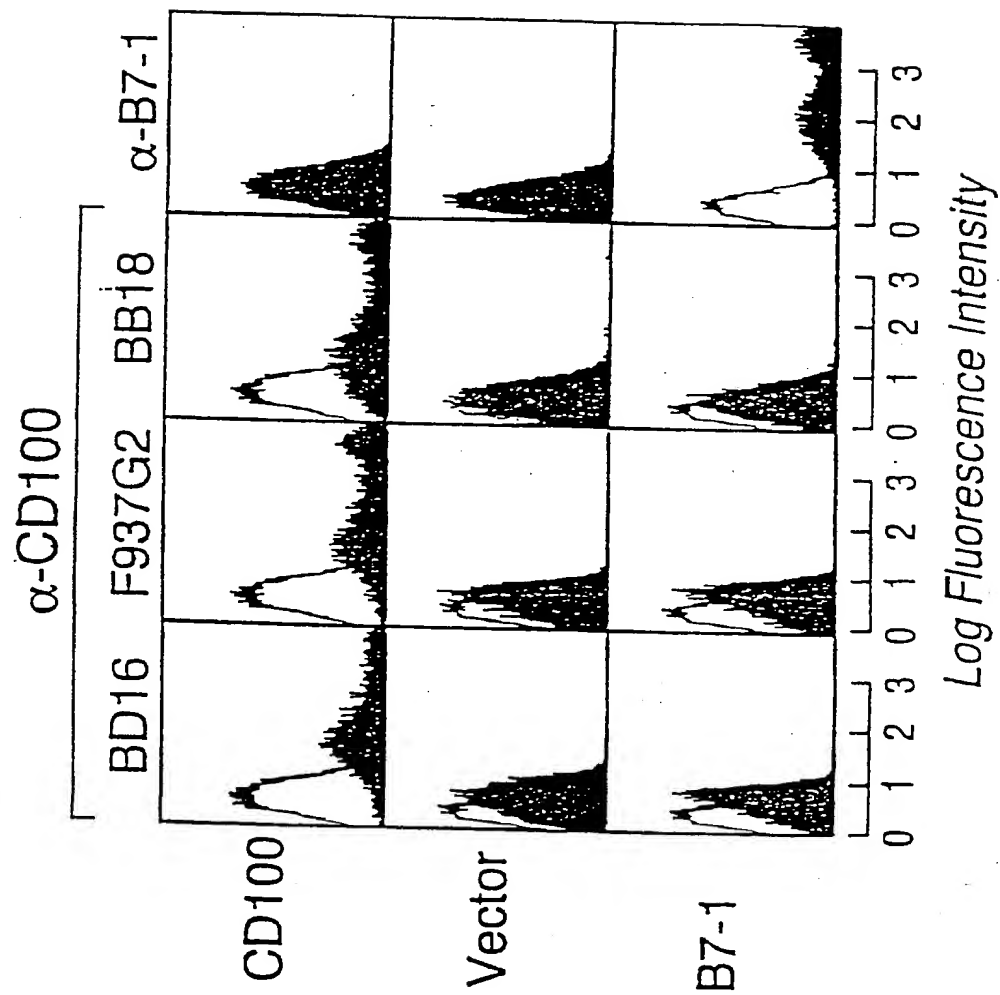
5/20

FIGURE 4

DDKIYFFFTTEVSVEYEFVVGKLMIPRIAR
GELYSGTSYNFLGSEPIISRNSSSHPLRTEYAI PWLNPSFVFADVIRKSPDSDGEDDRVYFFFTTEVSVEYEFVFRVLIPRIAR
VCKRDQGGRLTLQKKWTSFLKARLICTIPDKNLIFNIINDVFTLKSPTLKEPVIYGVFTPOLNNVGLSAVCAYNLSAVEEVFSKG
VCKGDOGGRLTLQKKWTSFLKARLICSRLPDSGLVFNVLRLDVFVLRSPGLKVPVFYALFTPOLNNVGLSAVCAYNLSTAEVFSHG
KYMOSATVEQSHTKWVRYNGEIPNPRPGACINNEARALNYVTSLNLPDKTLQFVKDHPMLDSDVT PVGDRPRLVKRDVKYTOIVV
KYMOSTTVEQSHTKWVRYNGFVFKPRPGACIDSEARAANYTSSLNLPDKTLQFVKDHPMLDSDVTPIINRPRLIKKDVNYTOIVV
DRVRLNCTIYDVMFISTDQALHKAISYENGHHII EETQLFPKFEPVOTLLSSKKSRRYLYAGSNSGVVQSPVAFCDTYTTCF
DRTQALDGTIVYDVHFVSTDRGALHKAISLEHAVHHII EETQLFQDFEPVOTLLSSKKGNRFVYAGSNSGVVQAPLAFCGKHGTCE
DCVLARDPYCAW
DCVLARDPYCAWSPTATCVALHQTESPSRGLIQEMSGDASVC PDKSKGSYRQHFFKHGCTAELKCSQKSNLARVFWKFGVGLK

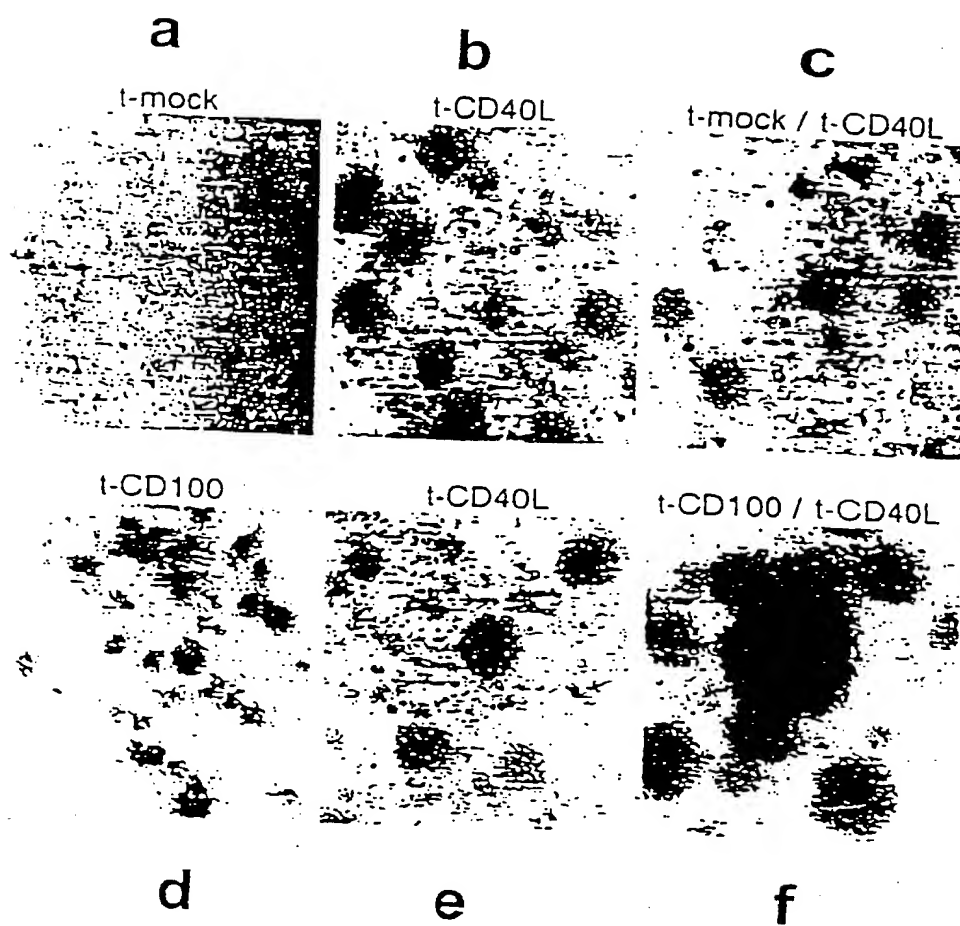
6/20

FIGURE 5



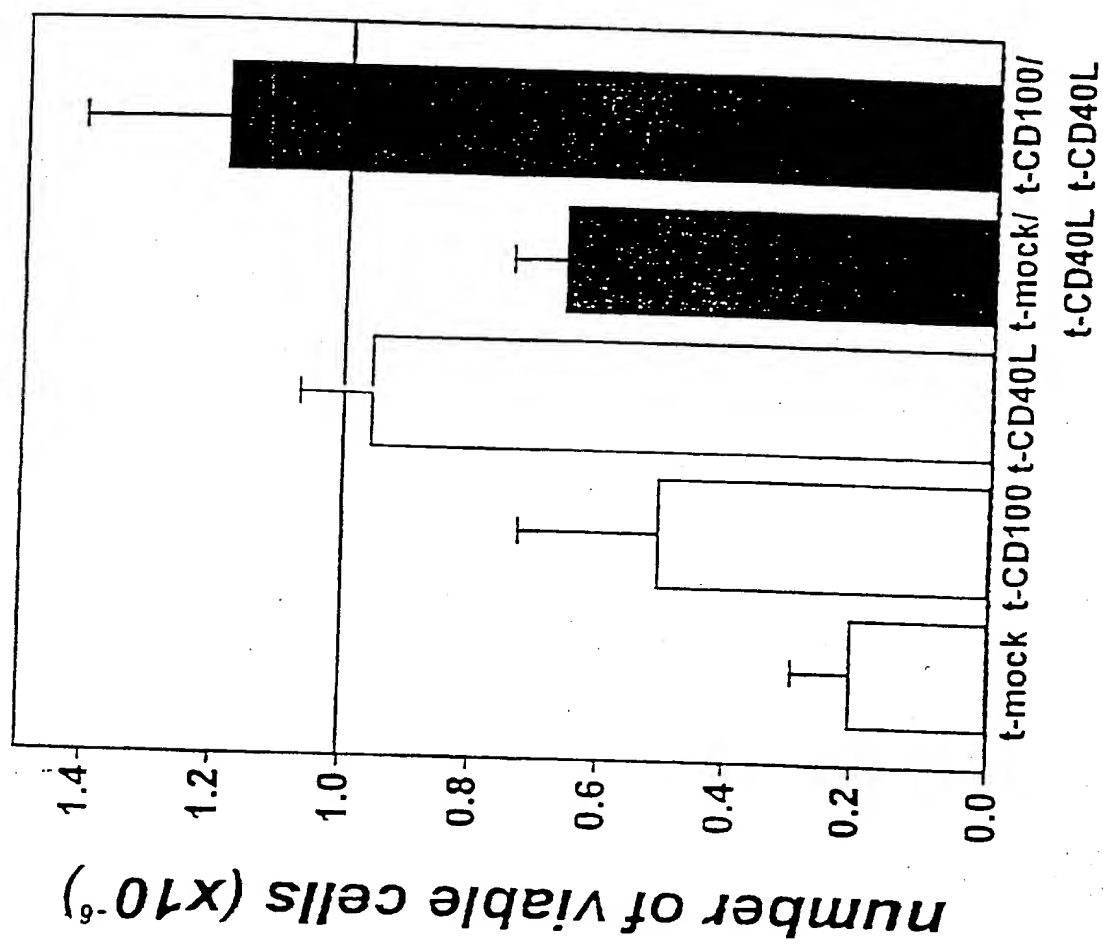
7/20

FIGURE 6



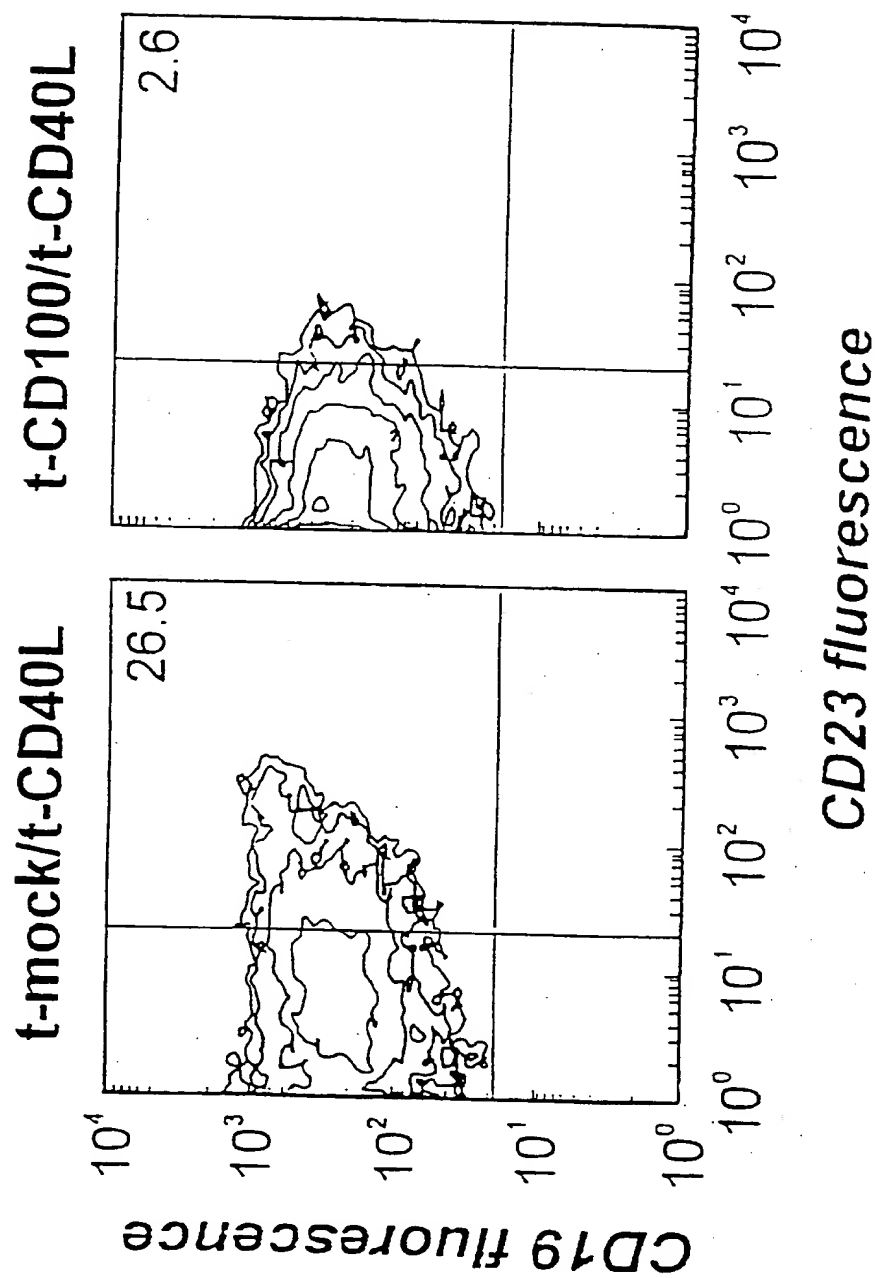
8/20

FIGURE 7



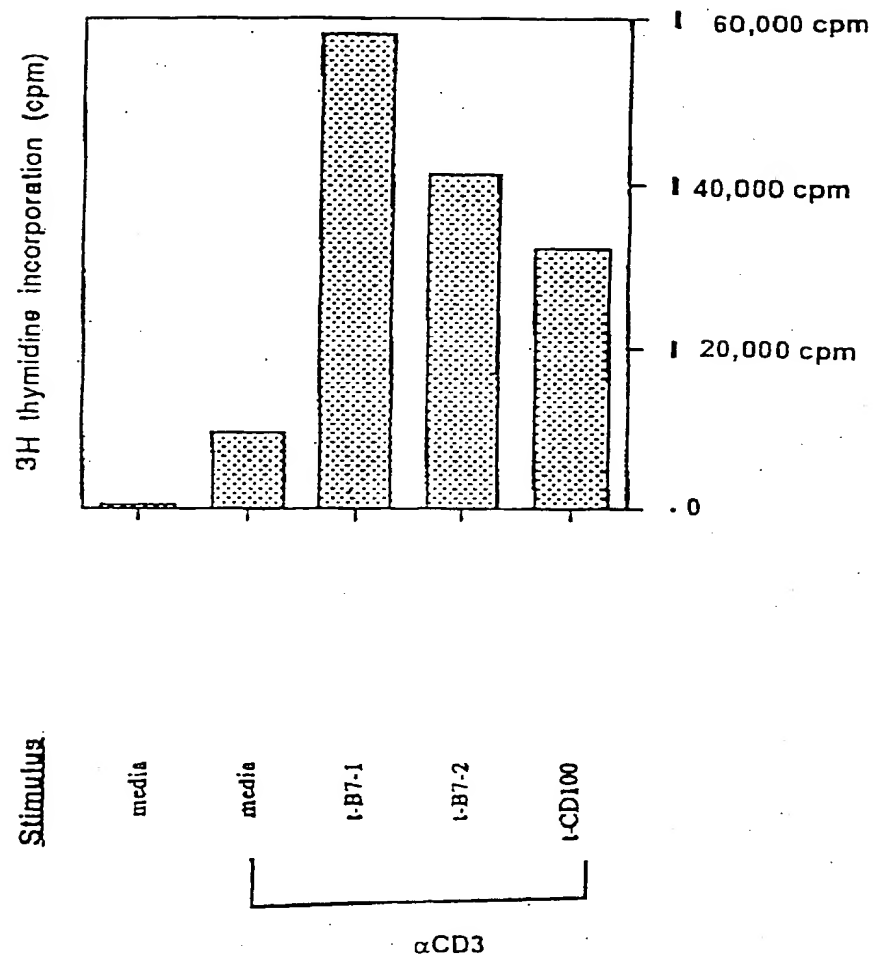
9/20

FIGURE 8



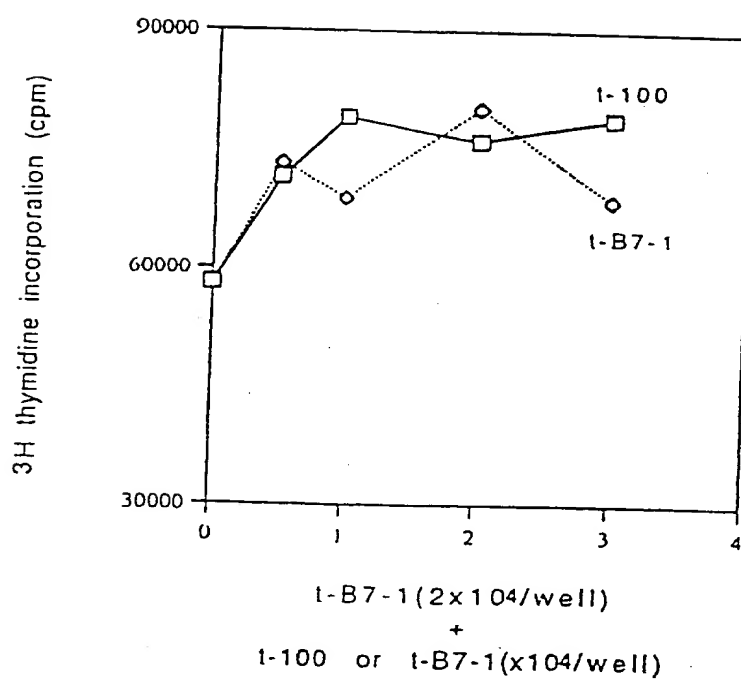
10/20

FIGURE 9



11/20

FIGURE 10



12/20

FIGURE 11

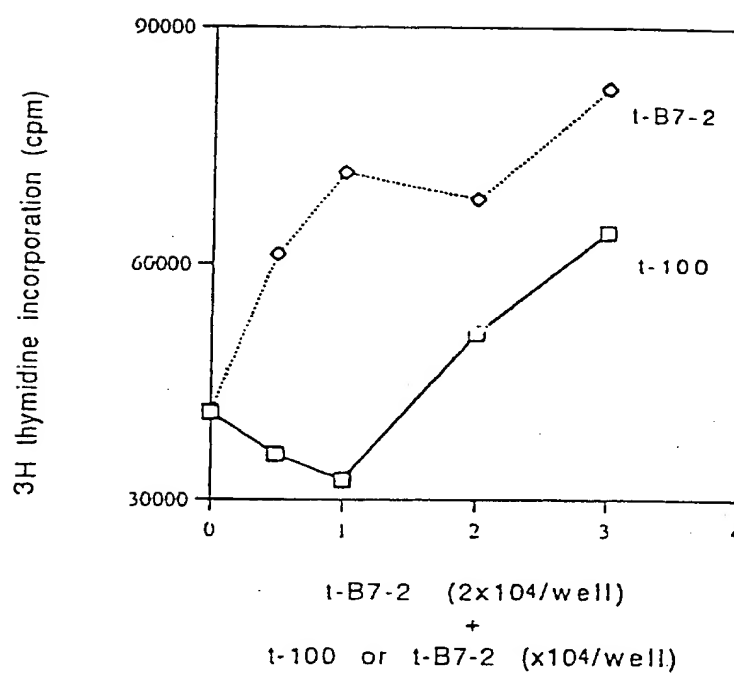


FIGURE 12

CATCTCCGCGCGTCTCCCGGCCCTCCCGGACTCAAGCTCCTGGCGCCGTTTCGCCTCTGTGCG
TCGCTGCCACCAACGCCGCCGCGCCATTCTTGGCGCGGAGCTGGCCTGGCCAGCCCCCGCCG
AGAGCCTCCGCGGGTCCGACGCGCGCTCCAGACCCTGGTAACACCACAGGAACACAGCCA
AGTCTCTGAATACCGACATGTCTGACAGTGTGATCCCTAGGTGACACGGGAACACCGGCA
GCCTTGGCATGACGTCGTGAAGGTGGCCATTGCTAACCTGACATGTGGGGACTCAGGAAC
CCCACCCCTTATGGGCTCCAGTCTGTGCTGCTGGCCCCAGCTCTGGGGCTCTAAGAGGTC
CTTGCTGCTACCCACAGCAGCCTGTGCCATCCATGTGTGCCCGTTGCTGAAGGCCTCG
GTGGCCCCCTGCCCATGAGGATGTGTGCCCGCCGTTAGGGGGCTGTTCTTGGCCCTGGTGGT
AGTGTGAGAACC CGGTGGCATTTCACACCTGTGCCTCGGCTCACCTGGGAACATGGAGA
GGTAGGTCTGGTGCAGTTTACAAGCCAGGCATCTTTAACTACTCGGCCTTGCTGATGAG
TGAGGACAAAGACACTCTGTATGTAGGCGCCCGGAAGCAGTCTTTGCAGTGAATGCGCT
GAACATCTCTGAGAAGCAACATGAGGTATATTGGAAGGTCTCTGAAGACAAAATCCAA
GTGTGCAGAGAAGGGGAAATCAAAGCAGACGGAATGCCTAACTACATTTCGAGTACTACA
GCCACTAAGCAGCACTTCCCTCTATGTGTGTGGGACCAATGCGTTCCAGCCCACCTGTGA
CCACCTGAACCTTGACATCCTTCAAGTTTCTGGGGAAAAGTGAAGATGGCAAAGGAAGATG
CCCCTTCGACCCCCGCCACAGCTACACATCAGTCATGGTTGGGGGCGAGCTCTACTCTGG
GACGTCTATAATTTCTTGGGCAGTGAACCCATCATCTCTCGAAACTCTTCCCACAGTCC
CTTGAGGACGGAGTATGCCATCCCGTGGCTGAACGAGCCTAGCTTCGTCTTTGCTGACGT
GATCCAGAAAAGCCCAGATGGTCCGGAGGGTGAAGATGACAAGGTCTACTTCTTTTTTAC
GGAGGTATCCGTGGAGTACGAATTCGTCTTCAAGTTGATGATCCCGCAGTTGCCAGGGT
GTGCAAGGGCGACCAGGGCGGCCTGCGGACTTTGCAAAAAAAGTGGACCTCCTTCTTAAA
GGCCAGGCTGATCTGCTCCAAGCCAGACAGTGGCCTGGTCTTCAACATACTTCAGGATGT
GTTTGTGCTGAGGGCCCCGGGCCTCAAGGAGCCTGTGTTCTATGCGGTCTTACCCCCACA
GCTGAACAATGTGGGTCTGTACGCGGTGTGCGCCTACACACTGGCCACGGTGGAGGCAGT
CTTCTCCCGTGGAAAGTACATGCAGAGTGGCACAGTGGAGCAGTCTCACACCAAGTGGGT
GCGCTACAATGGCCCAGTGCCCACTCCCCGAGCAGACAAAACACTGCAGTTTGTAAGAA
GGCAGCCAACTACACCAGCTCCTTGAATCTCCAGACAAAACACTGCAGTTTGTAAGAA
CCACCCTTTGATGGATGACTCAGTGACCCCGATAGACAAACAGACCCAAAGCTGATCAAAAA
AGATGTAAACTACACCAGATAGTGGTAGACAGGACCCAGGCCCTGGATGGGACTTTCTA
CGACGTCACTGTTTCATCAGCACAGACCGGGGAGCTCTGCATAAAGCAGTCACTCACA
AGAGGTGCATGTCTCATCGAGGAGACCCAACTCTTCCGGGACTCTGAACCGGTCCTAACTCT
GCTGCTATCGTCAAAGAAGGGGAGGAAGTTTGTCTATGCAGGCTCCAACCTCTGGAGTGGT
CCAAGCGCCCCCTGGCATTCTGCGAAAAGCACGGTAGCTGTGAAGACTGTGTGTTAGCACG
GGACCCCTACTGTGCCTGGAGCCCAGCCATCAAGGCCTGTGTTACCCTGCACCAGGAAGA
GGCCTCCAGCAGGGGCTGGATTCAAGGACATGAGCGGTGACACATCCTCATGCCTGGATAA
GAGTAAAGAAAGTTTCAACCAGCATTTTTTCAAGCACGGCGGCACAGCGGAACCTCAAATG
TTTCCAAAAGTCCAACCTAGCCCCGGGTGGTATGGAAGTTCCAGAATGGCGAGTTGAAGGC
CGCAAGTCCCAAGTACGGCTTTGTGGGCAGGAAGCACCTGCTCATCTTCAACCTGTCCGA
CGGAGACAGCGGCGGTGTACCAAGTGCCTGTGAGAGGAAAGGGTGAAGGAATAAACGGTCTC
CCAGCTGTGGCCAAAGCACGTTCTGGAAGTGAAGATGGTACCTCGGACCCCCCCCCCTCACC
TACCTCAGAGGATGCTCAGACAGAAGGTAGTAAGATCACATCCAAAATGCCGGTTGCATC
TACCCAGGGGTCTCTCCCCCTACCCCGGCTCTGTGGGCAACCTCCCCAGAGCCGCCAC
CCTACCTCCCAAGTCTCTCTCCGGCACATCCTGTGAACCAAGATGGTCAACACGGT
CCCCAGCTCCACTCAGAGAAGACGGTGTATCTCAAGTCCAGTGACAACCGCCTGCTCAT
GTCTCTCTCTCTCTTTCATCTTTGTCTCTTCTCTGCTCTTTTCTTCAACTGCTACAA
GGGTACCTGCCCCGACAGTGTCTTAAATTCGGCTCAGCCCTGCTGCTTGGAAAGAAAAC
ACCCAAGTCAAGTCTCTGACCTGGAGCAGAGTGTGAAGGAGACACTGGTTCGAGCTGG
GAGCTTCTCCAGCAGAACGGCGACACCCCAAGCCAGCCCTGGATACGGGCTATGAAAC
GGAGCAGGACACCATCACCAGCAAAGTCCCCACGGATCGTGAGGACTCGCAACGGATCGA
TGAACCTCTGCCCCGGGACAAAACCGTTTGATGTCAAGTGTGAAGTGAAGTTTGCAGATTC
GGATGCTGACGGGGACTGAGGCCAGCGTGTCCAGCCCATGCCCTCTGTCTTCTGTTGGAG
AGTGTGTGTTGAGCCCATTCAGTAGCCGAGTCTTGTCACTCTGTGCCAGCCTCAGTCTT
GTGTCCCTTTTTCTCTTGGGTTGAGCCTGTGGCTCATCCCCCTTGTCTTTTGGGAAGCA
AGTATCTATTCCAGTCTCAAGTCTGCAGTTGCTGGAGCGCTTACGCACCTGAGCCCTT

FIGURE 12 (CONTINUED)

GTGTCCTGGGGGAGAGATGGCCACCTCCGTGGGCTGCGAAGAGCCACCCCTTCCTCTTCC
GATTCTCCTAGCAGCCACTCAGAGATAATTTAATTCCAGATTGGAAACGCCCTTTTAGTT
TATCAGATTGGTAACTTACATCCTGCTGCCCAGATGGCACGGACAGTTTTCTTTCACTTA
ATTATTATTTTTTTTTTAAGGATTTTCGCTCCTATTGTGTTGATGTCTTAGGTCATTTTC
TTTTTTCTTTCTCTTTTTTTATTACCAGAGGAGATGTTTAAATATTCATGAGAAGAGGA
ACATTTTCTAGATTTTTTTGTGTTATATATTGAGATATAAAATATGGCTATGTTGCTTA
AGATTCTCAGGGATAGACTTATTTTTGTAACTTCATTCTTTCCTGCTGTTAGGAACATA
GGCCTAAAATTGTCTCTTGAGTTTGCTCACCCCTTTGTTTTGGTAGGGTTTTTTTGTTGT
TGCTGTTATTGTTTCTAGTTTTTAATCTTATTCATTTTGAAGGATTTTCTTTCTGAACT
TTTTAAATTTTTATATTTTCTGCCATACATCTACAAAGTGGGTTTTGAGTGAGGGCAGG
TGGCCCAGTGGCTTTGGGTGGCGACTGAGCTGGTCCCACGAGGGGAGGAGGGTTATATA
CCCCATGACCCTGCGGCTTCTTGGCGCCTCCTGCCCATGAGGATCACATCCTGTCTCTCC
TTGCTTCCATCTCTCATCACTGCCCTTGGACTTCCGCCTTGACTGTCCATGAAAGACAGA
AATGGGTGGGTAGTTGGGCTCCCAACCTCGGATGGTGACCGCAANATCCCGNGTGGGCG
GCCGGCCGNTCNTGCAGCCCGANTNTCCTGCCAGTGTNTTTCAGGATGTNAACGGGNGGT
ACGATTNTGGCATTGTTTTTTCGCTCNCNGNGTGGAANANTCATTCCATGTNGNGGN
GACGAATTTTGGATTCCCCCCCCACCCCGNGCGNGTAGANAATNNTTTTTTGCA
TGACANGATTACCATTCGGTGTAANATTTGNGTTTATAAGATTTANTTTGTTTTATT
TTTTTANTNGNACTGTANANATTTGNAAAGTACCCAAATAAACCGNAGNTTTNTNAAA
AA

15/20

FIGURE 13

*** Aligned sequences:
 C1 (1f): |>u 1>+++++ murineCD100 (4470 bases)++++>u 4470>|
 C2 (1f): |>u 88>+++++humanCD100coding region (2589 bases)++++>u 2676>|

*** Alignment of first sequence with all others displayed
 *** Key:

UPPER CASE = aligned non-identical bases
 lower case = unaligned bases
 ----- = aligned identical bases
 = gap

```

mod2c-106 : GTGGCCCCCTGCCCATGAGGATGTGTGCCCCCGTTAGGGGGCTGTTCTTGGCCCCCTGGTGGT
cd100 : .....-CA-----A-----C-A-----T-CA--

mod2c-106 : AGTGTGAGAAACCGCGGTGGCATTTCACCTGTGCCTCGGCTCACCTGGGAACATGGAGA
cd100 : GA-----TG-G--A--A-----CA-A--C--A-----G-CA--

mod2c-106 : GGTAGGTCTGGTGCAGTTTCACAAGCCAGGCATCTTTAACTACTCGGCCTTGCTGATGAG
cd100 : ---GCAC-----TG-----A-----AC-----A-----C--

mod2c-106 : TGAGGACAAAGACACTCTGTATGTAGGCGCCCGGAAGCAGTCTTTGCAGTGAATGCGCT
cd100 : C-----G-----CT---CA---T-----G--G-----C--T---C--A--

mod2c-106 : GAACATCTCTGAGAAGCAACATGAGGTATATTGGAAGGTCTCTGAAGACAAAAATCCAA
cd100 : C-----C-----G-----G-----A-----G-A--

mod2c-106 : GTGTGCAGAGAAGGGGAAATCAAAGCAGACGGAATGCCTAAACTACATTGAGTACTACA
cd100 : A-----A-----A-----A-----C-----C--G--G--G--

mod2c-106 : GCCACTAAGCAGCACTTCCCTCTATGTGTGTGGGACCAATGCGTTCCAGCCCACTGTGA
cd100 : -----C--GC-----T--C-----C--A-----GG-----

mod2c-106 : CCACCTGAACTTGACATCCTTCAAGTTTCTGGGGAAAAGTGAAGATGGCAAAGGAAGATG
cd100 : -----A-----T-----A-----

mod2c-106 : CCCCTTCGACCCCGCCACAGCTACACATCAGTCATGGTTGGGGGCGAGCTCTACTCTGG
cd100 : T-----T-----A--A-----C-----AT--A--A--T--T--G--

```

FIGURE 13 (CONTINUED)

mod2c-106 : GACGTCCTATAATTCTTGGGCAGTGAACCCATCATCTCTCGAAACTCTTCCCACAGTCC
cd100 : -----G-----T-----A-----C-----T-----
mod2c-106 : CTTGAGGACGGAGTATGCCATCCCGTGGCTGAACGAGCCTAGCTTCGTCTTTTGCTGACGT
cd100 : TC-----A--A-----A-----T-----T-----G-----
mod2c-106 : GATCCAGAAAAGCCCAGATGGTCCGGAGGGTGAAGATGACAAGGTCTACTTCTTTTTTAC
cd100 : -----GA-----CA-C--C--C--C--G-----G-----C--C--
mod2c-106 : GGAGGTATCCCGTGGAGTACGAATTCGTCTTCAAGTTGATGATCCCGGAGTTGCCAGGGT
cd100 : -----G--T-----T--G--T--G--G--G--C-----A--GA-A--A--A--
mod2c-106 : GTGCAAGGGCCAGCCAGGGCGGCTGCGGACTTTGCAAAAAAAGTGACCTCCTTCCTAAA
cd100 : -----G-----A--C-----G--G--A-----G--
mod2c-106 : GGCCAGGCTGATCTGCTCCAAGCCAGACAGTGGCCTGGTCTTCAACATACTTCAGGATGT
cd100 : A--C-A--C-----CG-----C--T-----TG-G--G--G--
mod2c-106 : GTTTGTGCTGAGGGCCCCGGGCTCAAGGAGCCTGTGTTCTATGCGGCTTTCACCCACACA
cd100 : C--C-----C--T-----G-----T-----AC-----
mod2c-106 : GCTGAACAATGTGGTCTGTCAGCGGTGTGCGCCTACACACTGGCCACGGTGGAGGGCAGT
cd100 : -----C-----G-----G--A-----AC--T--A--CC--AG--
mod2c-106 : CTTCTCCCGTGCAAAGTACATGCAGAGTGCCACAGTGGAGCAGTCTCACACCAAGTGGGT
cd100 : -----AC--G-----CA-----C-----
mod2c-106 : GCGCTACAATGGCCCCAGTGGCCACTCCCCGACCTGGAGCGTGTATCGACAGTGAAGCCCCG
cd100 : -----T-----G--A--AG--G--G-----C-----C--A--
mod2c-106 : GGCAGCCAACCTACACCAGCTCCTTGAATCTCCCAGACAAAACACTGCAGTTTGTAAAAGA
cd100 : --C-----T-G-----G--G-----C--T--
mod2c-106 : CCACCCTTTGATGGATGACTCAGTGACCCCGATAGACAACAGACCCCAAGCTGATCAAAAA
cd100 : -----G--A--A-----G-----G--T-A-----G--
mod2c-106 : AGATGTAACTACACCCAGATAGTGGTAGACAGGACCCAGGCCCTGGATGGGACTTTCTA
cd100 : -----G-----C-----G--C-----G-----
mod2c-106 : CGACGTCATGTTTCATCAGCACAGACCGGGAGCTCTGCATAAAGCAGTCATCCTCACAAA
cd100 : T--T-----TG-----C-----CA--G-----GAGC--
mod2c-106 : AGAGGTGCATGTCATCGAGGAGACCCAACTCTTCCGGGACTCTGAACCGGTCTTAAGTCT
cd100 : C-CT--T--CA-----G-----A-----T--G--A--AG--C--
mod2c-106 : GCTGCTATCGTCAAAGAAGGGGAGGAAGTTTGTCTATGCAGGCTCCAAGTCTGGAGTGGT
cd100 : -----G--T-----C-AC-G-----T-----T-----G--C-----
mod2c-106 : CCAAGCGCCCTGGCATTCGCGAAAAGCACGGTAGCTGTGAAGACTGTGTGTTAGCAGC
cd100 : --G--C--G-----C-----T-GG-----C--C--C--G-----C--G--G--
mod2c-106 : GGACCCCTACTGTGCTGGAGCCAGCCATCAAGGCTGTGTTACCTGACACAGGAAGA
cd100 : -----C-----GC--CAGC-A--C--GG-T-----ACC--
mod2c-106 : GGCCTCCAGCAGGGGCTGGATTCAAGACATGAGCGGTGACACATCCTCATGCCCTGGATAA
cd100 : -AG-C-----T-T-----G-----C--TG-T--TG-T--C-----

FIGURE 13 (CONTINUED)

```
mod2c-106 : GAGTAAAGAAAAGTTTCAACCAGCATTTTTTCAAGCACGGCGGCACAGCGGAACCTCAAATC
cd100 : A-----G-----A-CGG-----T-----G-----

mod2c-106 : TTTCCAAAAGTCCAACCTAGCCCGGGTGGTATGGAAGTTCCAGAATGGCGAGTTGAAGGC
cd100 : C-C-----A-----G-----CT-T-----T-----

mod2c-106 : CGCAAGTCCCAAGTACGGCTTTGTGGGCAGGAAGCACCTGCTCATCTTCAACCTGTCCGA
cd100 : --AG--C-----TC--A-----A--AA--T-----T---A--

mod2c-106 : CGGAGACAGCGGCGTGTACCAGTGCCTGTCAGAGGAAAGGGTGAGGAATAAAACGGTCTC
cd100 : A-----T--G-----G-----T-A--C-----T

mod2c-106 : CCAGCTGCTGGCCAAGCACGTTCTGGAAGTGAAGATGGTACCTCGGACCCCCCTCACC
cd100 : --AG--G-C-----C-----G---T---AAA-C---GTAGTGG-C--

mod2c-106 : TACCTCAGAGGATGCTCAGACAGAAGGTAGTAAGATCACATCCAAAATGCCGGTTGCATC
cd100 : C----TGTCA-T--T-----G---TG-CA-----G--TT---G-----

mod2c-106 : TACCCAGGGTCTCTCCCCCTACCCCGGCTCTGTGGGCAACCTCCCCAGAGCCGCCAC
cd100 : C----A-----T-----A-----A--CG--CA--C-----T--G-G---AT---

mod2c-106 : CCTACCTCCCAAGTCCT...CCTCCGGCACATCCTGTGAACCAAGATGGTCATCAACA
cd100 : ---T-----g-c-g-c--A-----C-----C-----

mod2c-106 : CGGTCCCCCAGCTCCACTCAGAGAAGACGGTGTATCTCAAGTCCAGTGACAACCGCCTGC
cd100 : -----G-----A--CA-----T-----C-----C-

mod2c-106 : TCATGTCTCTCCTCTCTTCATCTTTGTCTCTTCTCTGCCTCTTTTCTACAACTGCT
cd100 : -----C--T-----T-----T-----T-----

mod2c-106 : ACAAGGGCTACCTGCCCGGACAGTGCCTTAAATTCGGCTCAGCCCTGCTGCTTGGAAAGA
cd100 : -T-----A-----A-----G-----G-----A--AA---G-----

mod2c-106 : AAACACCCAAGTCAGACTTCTCTGACCTGGAGCAGAGTGTGAAGGAGACACTGGTCGAGC
cd100 : -G-AG-----T---G-----GT-----CC-----GT-A--A---

mod2c-106 : CTGGGAGCTTCTCCCAGCAGAACGGCGACCACCCCAAGCCAGCCCTGGATACGGGCTATG
cd100 : -A-----T--G--G-----C-----C-----

mod2c-106 : AAACGGAGCAGGACACCATCACCAGCAAAGTCCCCACGGATCGTGAGGACTCGCAACGGA
cd100 : -G--C-----A-----A-G-----A--GA---

mod2c-106 : TCGATGAACTCTCTGCCCCGGGACAAACCGTTTGATGTCAAGTGTGAAGTGAAGTTTGCAG
cd100 : ---C--C--T-----A-----G--C-----C-----G-----C--T-

mod2c-106 : ATTCCGATGCTGACGGGGACTGAGGCCAGCGTGTCCCAGCCCATGCCCCCTGTGTCTTCGT
cd100 : -C--A--C--A--T--A-----
```

FIGURE 14

1: MRMCAFVRGLFLALVVVLR TAVAFAPVPRLTWEHGEVGLVQFHKPGIFNYSALLMSEDKD
61: TLYVGAREAVFAVNALNISEKQHEVYWKVSEDKSKCAEKGKSKQTECLNYIRVLQPLSS
121: TSLYVCGTNAFOPTCDHLNLT SFKFLGKSEDGKGRCPFDP AHSYTSVMVGGELYSGTSYN
181: FLGSEPIISRNSSHSPLRTEYAIPWLN EPSFVFADVIQKSPDGPEGEDDKVYFFFTESV
241: EYEFVFKLMIPRVARVCKGDQGG LRTLQKKWTSFLKARL ICSKPD SGLVFNILQDVFVLR
301: APGLKEPVFYAVFTPQLNNVGLSAVCAYTLATVEAVFSRGKYM QSATVEQSHTKWVRYNG
361: PVPTPRPGACIDSEARAANYTSS LNLDPKTLQFVKDHP LMDDSVTPIDNRPKLIK KDVNY
421: TQIVVDRTQALDGT FYDVMFISTDRGALHKAVILTKEVHV IEETQLFRDSEPVL TLLLSS
481: KKGRKFVYAGSNSGVVQAPLAFCEKHGSCEDCVLARDPYCAWSPA IACVTLHQEEASSR
541: GWIQDMSGDTSSCLDKSKESFNQHFFKHGGTAE LKCFQKSNLARVVWKFQNGELKAASPK
601: YGFVGRKHLLIFNLSDGDSGVYQCLSEERV RNKTVSOLLAKHVLEV KMPRTPPSP TSED
661: AQTEGSKITSKMPVASTQGSSPPTPALWATSPRAATLPPKSSSGTSC EPKMVINTVPOLH
721: SEKTVYLKSSDNRL LMSLLLFIFVLFLCLFSYNCYKGYLPGQCLKFRSALLLGK KTPKSD
781: FSDLEQSVKETLVEPGSFSQONGDHPK PALDTGYETEQDTITSKVPTDREDSQRIDELSA
841: RDKPFDVKCELKFADSDADGD

19/20

FIGURE 15

** Homology domain #1 (SD_Score = 11.1 / % = 68.3 / length = 41):

Signal peptide

```
mCD100    1 - MRMCAFVRGL FLALVVVLRT AVAFAPVPRL TWEHGEVGLV Q
          |||| |*||| **|| |** | |*|||*||* |||| || || |
hCD100    1 - MRMCTPIRGL LMALAVMFGT AMAFAPIPRI TWEHREVHLV Q
```

** Homology domain #2 (SD_Score = 50.6 / % = 88.5 / length = 512):

Sema domain

```
mCD100 42 - FHKPGIFNYS ALLMSEDKDT LYVGAREAVF AVNALNISEK QHEVYWKVSE DKKSCKAEKG
          || | |*||| |||*||| ||*||| ||||| ||||| ||||| ||| |||||
hCD100 42 - FHEPDIYNYS ALLLSEDKDT LYIGAREAVF AVNALNISEK QHEVYWKVSE DKKAKCAEKG

102 - KSKQTECLNY IRVLQPLSST SLYVCGTNAF QPTCDHLNLT SFKFLGKSED GKGRCPFDPA
      ||||| ||||| | ||||| || ||||| ||||| || ||||| ||
102 - KSKQTECLNY IRVLQPLSAT SLYVCGTNAF QPACDHLNLT SFKFLGKNED GKGRCPFDPA

162 - HSYTSVMVGG ELYSGTSYNF LGSEPIISRN SSHSPLRTEY AIPWLNPSF VFADVIQKSP
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||
162 - HSYTSVMVDG ELYSGTSYNF LGSEPIISRN SSHSPLRTEY AIPWLNPSF VFADVIRKSP

222 - DGPEGEDDKV YFFFTSVSVE YEFVFKLMIP RVARVCKGDQ GGLRTLQKKW TSFLKARLIC
      | |*|||*| ||||| |||||**|| |*||| ||||| ||||| |||
222 - DSPDGEDDRV YFFFTSVSVE YEFVFRVLIP RIARVCKGDQ GGLRTLQKKW TSFLKARLIC

282 - SKPDSGLVFN ILQDVFLRA PGLKEPVFYA VFTPQLNNVG LSAVCAYTLA TVEAVFSRGK
      |*||| ||||| *| ||||| ||||| ||||| *||| ||||| ||||| | | |||*||
282 - SRPDSGLVFN VLRDVFVLR S PGLKVPVFYA LFTPQLNNVG LSAVCAYNLS TAEVFSHGK

342 - YMQSATVEQS HTKWVRYNGP VTPRPGACI DSEARAANYT SSLNLPDKTL QFVKDHPLMD
      |||| |||| ||||| || ||||| ||||| ||||| ||||| |||||
342 - YMQSTTVEQS HTKWVRYNGP VPKPRPGACI DSEARAANYT SSLNLPDKTL QFVKDHPLMD

402 - DSVTPIDNRP KLIKDVNYT QIVVDRTQAL DGTFFYDMFI STDRGALHKA VILTKEVHVI
      ||||| ||||| *||| ||||| ||||| ||||| ||||| * ||||| ||*|
402 - DSVTPIDNRP RLIKDVNYT QIVVDRTQAL DGTVDYDMFV STDRGALHKA ISLEHAVHII

462 - EETQLFRDSE PVLTLILLSSK KGRKFVYAGS NSGVVQAPLA FCEKHGSCED CVLARDPYCA
      ||||| || ||||| || ||||| || ||||| ||||| || ||||| |||||
462 - EETQLFQDFE PVQTLILLSSK KGNRFVYAGS NSGVVQAPLA FCGKHGTCED CVLARDPYCA

522 - WSPAIAKACVT LHQEEASSRG WIQDMSGDTS SC
      ||| || ||| ||| ||*||| |||
522 - WSPPTATCVA LHQTESPSRG LIQEMSGDAS VC
```

FIGURE 15 (CONTINUED)

• Homology domain #3 (SD_Score = 15.9 / % = 85.5 / length = 76):

Ig domain

```

MCD100 555 - DKSKEFNFQH FFKHGCTAEL KCFQKSNLAR VVWKFQNGEL KAASPKYGFV GRKHLLIIFNL
          ||||| |* || ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| |||||
hCD100 555 - DKSXGSIYQH FFKHGCTAEL KCSQKSNLAR VFWKFQNGVL KAESPXYGLM GRKNLLIIFNL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
615 - SDGDSGVYQC LSEERV
          |*||| ||||| |||||
615 - SEGDSGVYQC LSEERV

```

```
** Homology domain #4 ( SD_Score = 14.1 / t = 70.9 / length = 103 ) :
```

Stalk domain

```
mCD100.63 - RNKTVSQLLA KHVLEVKMVP RTPPSPTSED AQTEGSKITS KMPVASTQGS SPPTPALWAT  
          * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| *  
hCD100.74 - KNKTVFQVVA KHVLEVKVVP KPVVAPTLVS VQTEGSRIT KVLVASTQGS SPPTPAVQAT  
  
29 - SPRAATLPPK .SSSGTSCEP KKVINTVPOL HSEKTYVYLS SDN  
   | | |||||      ||||| |*||||||| |||||*||| |||  
69 - SSGAITLPPK PAPTGTSCPEP KIVINTVPOL HSEKTHYLKS SDN
```

Homology domain #5 (SD_Score = 9.7 / λ = 84.2 / length = 19):

Transmembrane domain

```
mCD100 734 - LLMSLLLFIF VLFLCLFSY
          | | | | * | | | | | | |
hCD100 735 - LLMSLFLFFF VLFLCLFFY
```

```
** Homology domain #6 ( SD_Score = 21.1 / i = 92.8 / length = 111 );
```

Cytoplasmic domain

```

MCD100 753 - NCYKGYLPQO CLKFRSALLL GKTKPKSDFS DLEQSVKETL VEPGFSFSQON GDHPKPALDT
             ||||| | |||||* ||| ||||| ||||| |||||
HCD100 754 - NCYKGYLPQO CLKFRSALLI GKKKPKSDFC DREQSLKETL VEPGFSFSQON GEHPKPALDT
             ||||| | ||||| ||||| ||||| ||||| |||||
53 - GYETEQDTIT SKVPTDREDS QRIDELSARD KPFDVKCELK FADSDADGD
             ||||| | ||||| ||||| ||||| ||||| |||||
54 - GYETEQDTIT SKVPTDREDS QRIDDLWARD KPFDVKCELK FADSDADGD
             ||||| | ||||| ||||| ||||| ||||| |||||

```


INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 96/18645

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C07K 14/705

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C07K, A61K, C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPI, EPODOC, PAJ, MEDLINE, SCISEARCH, PCI, BIOSIS, DBA, GENBANK/EMBL/SWISSP
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C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Dialog Information Services, file 154, MEDLINE, Dialog accession no. 08854658, Medline accession no. 97030273, Hall KT et al: "Human CD100, a novel leukocyte semaphorin that promotes B-cell aggrega- tion and differentiation"; Proc Natl Acad Sci USA (UNITED STATES) Oct 15 1996, 93 (21) p11780-5 --	1-98
X	WO, A1, 9314125 (INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE), 22 July 1993 (22.07.93), page 4, line 10 - line 14, table 1, claims and the whole document --	1-98

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

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Date of the actual completion of the international search

26 February 1997

Date of mailing of the international search report

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 96/18645

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>Dialog Information Services, file 154, MEDLINE, Dialog accession no. 08225286, Medline accession no. 95234624, Herold C et al: "Activation signals are delivered through two distinct epitopes of CD100, a unique 150 kDa human lymphocyte surface structure previously defined by BB18 mAb"; Int Immunol (ENGLAND) Jan 1995, 7 (1) p1-8</p> <p style="text-align: center;">-- -----</p>	1-98

INTERNATIONAL SEARCH REPORT

Information on patent family members

03/02/97

International application No.

PCT/US 96/18645

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A1- 9314125	22/07/93	FR-A,B- 2686087 WO-A- 9318736	16/07/93 30/09/93